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Slobodyansky, Elizabeth Friday, February 25, 2005 9:40 PM STIC-Biotech/ChemLib

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Elizabeth Slobodyansky, PhD

Primary Examiner Art Unit 1652 **REM 2D83** 571-272-0941 MAILBOX 2C70

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Type of Search	
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ORGANISM RESULT 1 BD093238 LOCUS REFERENCE TITLE JOURNAL AUTHORS DNA encoding sucrose PTS enzyme II
Patent: WO 0102584-A 1 11-JAN-2001;
AJINOMOTO CO INC, MASAKO IZUI, MASAKAZU SUGIMOTO, TSUYOSH1
OS AMU KURAHASHI
OS Brevibacterium lactofermentum
PN WO 0102584-A/1
PD 11-JAN-2001
PF 30-JUN-2000 WO 2000JP004348
PR 02-JUL-1999 JP 99P 189512
PI MASAKO IZHI MASAKO-7777 DNA encoding sucrose PTS e BD093238 BD093238.1 GI:22638826 WO 0102584-A/1. unidentified unclassified. unidentified BD093238 5969 bp enzyme 5969 II. DNA SUGIMOTO, TSUYOSHI NAKAMATSU, linear PAT 27-AUG-2002

COMMENT

30-JUN-2000 WO 2000JP004348 02-JUL-1999 JP 99P 189512 MASAKO IZUI,MASAKAZU SUGIMOTO,TSUYOSHI NAKAMATSU,OSAMU

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C12N15/54, C12N9/12

KURAHASHI PC C12N CC FH Key FT CDS /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644" Location/Qualifiers Location/Qualifiers (3779). (5761).

FEATURES source

ORIGIN

닭 S Matches 5969; Query Match Best Local 9 Similarity AGTCCGTCGACGCCACCATTGATGTGGTGGTCACCGAGCTTGCGGAGGCTTTCTACATCT AGTCCGTCGACGCCACCATTGATGTGGTGGTCACCGAGCTTGCGGGAGGCTTTCTACATCT Conservative 100.0%; Score 5969; 100.0%; Pred. No. 0; Live 0; Mismatches DB 0; Length 5969; 0; Gaps 60 60

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                                    CACTAAGGCTGAGGATGGTTCCAATGTGGATATCTTGATGCACACTTGGTTTCGACACCGT
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Direct Submission

Submitted (24-MAY-2002) Satoshi Nakagawa, Kyowa Hakko Kogyo Co.

Ltd., Tokyo Research Laboratories; 3-6-6, Asahi-machi, Machida,

Tokyo 194-8533, Japan (B-mail:snakagawa@xanagen.com,

Tel:81-44-829-3031, Fax:81-44-813-1651)

This sequence is conducted by collaboration of Kyowa Hakko Kogy
                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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AP005282.1 GI:21325287
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188. 814
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                                                                                     'gene="Cg12516"
|88. .814
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QVSVTARECIGASR CEPIGEDC PAB I ARGKAKBADVVINHALLAI DALSDVSVILPEHD
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                                                                                                    complement (5587. .6312)
                                                                                                                                   TFLLYAYAFQTASGGPIMQRQ"
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9701. .10009
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                                                                                                                                                                                                                                                                         PTVNPCHRFHNSPRRGSIEWLRRPFQGRFLLKRDVPPRGPRGAWRSPTPICASEKPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="Cg12524"
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AAAACCCGGATTTCATTTTTCCCGGCAACCCAACAGATCTTGCCCGGGTGATCCATGCGG
                                                      TCCTGCTGTGCGGCATTCACCTCGAGGGCCCTTTCATCAACGCATGCCGTTGTGGTGCTC
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/gene="Cg12526"
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/gene="Cg12526"
/note="PF00210:Ferritin
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LNNLGYEGLFPADETKVSPNILSALSPNADENHDFFSGSGSSYVIGKAENTEDDDMDF
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CCTGATCCATACGAAGCAGCTGCAGAGTATGAGGCAAAGATCGCTGCAGAATCCGTTGAA 1919
                                                                                                                                                                                                                                                                                                                                                        ATCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGTTGCAGTCCTAATCGCACCCTTCGCC 1619
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149456 TATACCGCTCGACAGATCTTGAAAACTGGGAATTCTCCGGTGAAATCACCTTTGACCTCA 2939 GTGATGCACAACCTGGTTCTGCTCCTGATCTCCGGATGGCTACATGTGGGAATGCC	2879	2819 GTGATGGTTGGAACATGGTTCTTGGGGCCCAACGCGAAAACCTCACCGGTGCAGCGGTTC	2759 TCGACGGACCCGCCAGCGGTTTCACACCCCATTACCGCGATCCCATGATCAGCCCTGATG	2699 TCGAGGACCCAACTGGGCTGATGGGCGGCATTCATCGCCGTTCGCCCTAAAAATCCGCTT	2639 TCTACACCGGCAACCTAAAATTGACGGAAAGCGCCGCCACCCAAAACCTTGTCGAAG	6 9	2519 CCGGACCGCAGCGATTGCAGTGGACGCACCTGCCCGACGCTCTTTACCCGGATGCATCCT	2459 ATCCAGGTTTCCCCCTTCGCACCAAAGCGCACCGGCTGGGCTCACACCACCACCACGCCGTTGA	2399 TCAATGATCCCAACGGAATGTACGTCGATGGAGATACCCTCCACGTCTACTACCAGGACG	2339 TGCACACAAACTTTCCAGTTTGCGCCCTGCGTACCATGTGACTCCTCCGCAGGGCAGGC	2279 CGTCTCATGGAGCAATTAAAGCTGCGCTAGAAACAAAAAGGAAAGTACTGTGTGGGGCTA	2219 ATGCCACCATCATCGTTGGATGAAGCAGCAGTATCCAAGCTGGAAAACGCTGATCACTAC	2159 GGAACTGTGGAAGGCCCAGTGACTGCTTCTTGCCCAGGTTCCATCCTGTAGATGCACAAC	2099 TCCCGCGCGCAAAACATCGTGTTGGTGGCAACTGGTGAAGGAAAAAGCCGACGCCATCCGC	2039 TICTTCAACACCATCGAAGAGGTCCCAACCCACGCCGTCACCCAGGGTTTGGGCACTTTG	1979 CTGTCAGGACTGACAAAGGTCCAGGCGCTGCACCCTAAAACTGTGGAGGACAACGCTCGA	1920 GTTCAAATCCTTGGCATCGGCGGAAACGG-CACATCGCTTTCATTGAACCATCATCTTCT	76
CGGTGAAATCACCTTTGACCTCA 149397 CGATGGCTACATGTGGGAATGCC 2998	2938	AAACCTCACCGGTGCAGCGGTTC 2878	QY CGATCCCATGATCAGCCCTGATG 2818	A 2758 A 149577	2698 149637	2638 149697	2578 149757	2518 ·	2458 · 149877	2398	2338	2278 150057	2218 150117	2158 150177	2098 150237	2038 150297	1978	150
		3899 148437	3839 GTCGCCGCCGCACACTGTGCAACGCGTTTACGCCTCGTGCTCAAAGACACCCAAGGATGTG	148557 ATGGACCATAAGGACCTCGCGCAACGCATCCTGCGCGACATTGGCGGCGAAGACAACATT	3719 GCTTTTGAACAACATTCATGTCTGGATATTTTTGTTTCTTCCCGGTTAAGGAGAAATTC	3659 GTACAAATACTTCGCAAAATCCCTTGATCGGACAAATAAACAGGTTTAATATTCTTTA	148737	148796	1536 TIGGATICGIGATICGICGCGTAGCIGAGGTAAAACCTIGGCGGAATTAGTGATCGCGG 148856 TIGGATICGTGGTGATCGTCGCGTAGCTGAGGTAAAACCTGGCGAATTAGTGATCGCGG 148856 TIGGATICGTGGTGATCGTCGCGTAGCTGAGGTAAAACCTGGCGAATTAGTGATCGCGG	1419 CIGITCCGAGIAGACAICCGGAGCAAIAIIICCICCGAGIGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	148976 AAGAGCTTCTCCCCAGAGGGGGAGTCAGGGGTAATCAGATCTGTATTAGGTTCTGAAC	149036	3239 GCTCGTGGGCTGGATGGGCTGCCGCCAGGATGATCACCCAACAGTTGCACAGAAG	149156 AGCIGGATITCGGCCATGAATTCTACGCACCGCAGGTTGCAGTAAACGGTTCTGATGCCT	149216 GCGGATATGTCGCAAGCTTGAAGGAACGACCTTGCGACTAAACGATGCAATCAGCGTTGAAGGAATTCAGCGTTGAAGGAATTCAGCGTTGAAGGAACGACTTGAAGGAACGACTTGAAGGAATTCAGCGTTGAAGGAATTCAGCGTTGAAGGAATTCAGCGTTGAAGGAATTCAGCGTTGAAGGAATTCAGCGTTGAAGGAATTCAGCGTTGAAGGAATTCAGCGTTGAAGGAATTCAGCGTTGAAGGAATTCAGCGTTGAAGGAATTCAGCATGAAGGAATTCAGCATGAAGGAATTCAGCATGAAGGAATTCAGCATGAAGGAATTCAGCATGAAGGAATTCAGCATGAAGGAATTCAGAAGGAATTCAGAAGGAATTCAGAAGGAATTCAGAAGGAATTCAGAAGTAAAAACGAATTCAGAAGTAAAAAATTCAGAAGTAAAAAAAA	1119 GCGGATATGTCGACAAAGCTTTGAAGGAACGACGTTTCCGCGTCTTTGCGAGGATTTCAGCG	149336	2999

McHardy, A.C., Meyer, F.,	5159 TATGGCCTTTACTTGGTTCGCCGCAACGGCAGCATTGATCCAGATGCAACCGCTGCTCCA 5218	, V2
REFERENCE 1 (bases 1 to 349136) AUTHORS Kalinowski,J., Bathe,B. Burkovski,A., Dusch,N., Goesmann.A. Hartmann.M	5099 GTCATGTTCTTGGTTTGCGCGGTAGTTACCTTTGTCATCGCATTCGGCGCAGCGATTGCT 5158	B &
SOURCE Corynebacterium glutami ORGANISM Corynebacterium glutami Bacteria; Actinobacteri Corynebacterineae; Cory	5039 GCAGTTGCGTTGGGCGCTGCAGGTTTCTTGGGTGTTTCTATTGATGCTCCAGATATG 5098	Db Qy
complete genome BX927155 BX9271 BX927155.1 GI: complete genome	4979 TACATTGGTATCGGTACCGCAGCTATCGGTGGCGCTTTGATTGCACTCTTTGATATCAAG 5038	Db Oy
RESULT 3 EX927155/c BX927155 DEFINITION Corynebacterium glutami	4919 GTTCTTGGTATTACAGAGCCTGCGATCTTCGGTGTGAACCTTCGCCTGCGCTGGCCGTTC 4978	D Qy
146397	4859 TICTTCCTAGCGAAGAGTGAAAAGCTCAAGGGCCTTGCAGGTGCTTCAGGTGTCTCCGCT 4918	д Q
146457 T 5939 G	4799 TTCATCTTCGCAACCGCATCCATGGCCAATATATCGCGCAGGGTGCAGCATGTTTGGCAGTG 4858	ο Оу
146517	4739 ACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTCAACCAGGGTGGATCC 4798	D Qy
146577 5819	4679 GATTTCGGTGGTCCAGTCGGCGGTCTGCTTTTCGGTCTGGTCTACTCACCAATCGTTATC 4738	ρφ
146637 5759	4619 ATTGGTCCAGCAATGCGCTGGGTGGGTGACTTGCTGGCACACGGTCTGCAGGGACTCTAT 4678	Qy Db
146697 5699	4559 GACTTCCTGATCACCCCAGTGTTGACTCTGCTGCTCACCGGCTTCCTTACGTTCATTGCT 4618	Q y Db
146757 5639	4499 GTCTCTTGGATTCTGGCAATCGAGAAGTTCCTGCACAAGCGACTCATGGGCACTGCA 4558	Qy dd
146817 5579	4439 CIGITIGGITIGGAIGTIGCTCAAGCIGGTTACCAGGGCACCGIGCTICCIGIGCIGGIG 4498	οb
146877 5519	4379 CTGGTTAACGGCTACGACGTGGCCGCCACCATGACCGCGGGCGAAATGCCAATGTGGTCC 4438	ОУ
146937 5459	4319 CGTTTCGGTGGCAATGAGTTCCTGGGCGCCGGCATTGGTATGGCGATGGTGTTCCCCAACC 4378	Qy
146997 A 5399 G	4259 CTGATGGCATCTGCGCGTTCGTCGCGGTGGTTGGTTGGTT	Qу
147057	4199 GGTCCGCAATCACTGGTGGAGATGTTCCCTCAGATCAGCGGTGTTGCTGAGATGATCAAC 4258	Db Qy
147117	4139 TTGGTTGGCGGTCTGCTCATGGCTATCAACAATGTGTTGGTTG	da 40
Db 147177 TATGGCCTTTACTTGGTTCGC	4079 AACTGGTTCAGCCGTGCTGTGAAGGTATTGGCGGACATTTTCGTCCCGCTGATTCCAATC 4138	DD QQ

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	ROGGCGATGAAGCA

DEFINITION Corynebacterium glutamicum ATCC 13032, IS fingerprint type 4-5, accession Exp27155 asp27147
VERSION Exp27155 bsy27147
VERSION Exp27155 bsy27147
VERSION Exp27155 bsy27147
VERSION Expanse.

Complete genome.

Corynebacterium glutamicum ATCC 13032
Corynebacterium glutamicum ATCC 13032
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacterium.

Corynebacterineae; Corynebacterium.

REFERENCE (Corynebacterineae; Corynebacterium.

Corynebacterineae; Corynebacteriae; Bischoff,N., Bott,M., Bottels,D., Bischoff,N., Bott,M., Goesmann,A., Hartmann,M., Huthmacher,K., Kramer,R., Linke,B., McHardy,A.C., Meyer,F., Mockel,B., Pfefferle,W., Puhler,A.,

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REFERENCE
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join(BX927148.1:1. .348071, BX927149.1:51. .349887
BX927150.1:51. .34847.
BX927151.1:51. .349459, BX927152.1:51. .349799, BX9
BX927154.1:51. .34957, BX927155.1:51. .349136, BX9
BX927157.1:51. .140057)
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This sequence was accomplished by collaboration between
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Genomforschung, Universitaet Bielefeld; Universitaetsstrasse 25,
33615 Bielefeld, Germany
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Kalinowski,J.
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DKTVFGVTAALIAFIANGISSDDSVSSVSSTMESWAMINTGMUTHFVMLIGISDDTHYS
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NLTILIAIPFALVLIVMAIAFIKDLSTDPAAIRQRYAKAAISNAVVRGLEEHGDDFEL
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LVPGNHDSCHPMYRHAYKRQRRFLEVFDSVQAFQRMKWDDEDVYLSHFPRPGQDHPGM
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/locus_tag="cg2562"
                                                                                                                                                                     complement (3014.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MYYKQLDSLVFTDGESIAKARLASMTDMWFSSDLHLGHKFVASM/
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DAATNEGTSLNSAQVINGDCGDVNIPGESSSDNSSSDFATGSIAGAFATAVLAVVGIA
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ANTGVPTPGAGNVAAEGSGEEEGVVAAVAQLPFINVEITPIHLGGDFTGEDMSGVDFDA
NSTAWIANNDIGKIYSLAHDIANNTYKLTGEWETGYPEGGGEPDAEGIVAATNGDIYL
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4836. .6431
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3674. .4672
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/tzans1ation="MATTASKISTIRPAQQDALWSVREDLHARFDGLVDPVQVDAILD
HVASNREAKITVFSKIFIAREATAALQQIAGNVNADLLDFIALNRGMAA"
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/product="hypothetical protein predicted
;limmer/Critica"
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/codon_start=1
/transl_table=11
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/product="putative secreted protein"
/protein_id="CAR21001.1"
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                                                                                                                                                                                                              (product="PUTATIVE C4-DICARBOXYLATE TRANSPORT SYSTEM (FERMEASE LARGE PROTEIN)"
(protein_id="CAP21003.1"
(db_xref="GI:41326521"
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/locus
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/locus_tag="cg2571"
complement(9722. .11569)
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SATPLITYGEVTAMQSGVLDGA.EMUBLISYVTQMHFEVJARVNSTTUNLIVGLDYMVRHD
LLDAMSEPDRELFLEEMDAAMTEHTDLMVTETDAVIEKAKAGGAEFVEVDAQAFTDAL
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(PERWEASE SMALL PROTEIN)"
(perwease small protein)"
(pervease small protein)"
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(pervease small protein)"
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(db_xref="GI:41326522"
(translation="MMNFKSIVOTAMOVFSROVLHSPSTWSEELSKLLFVWLSFAGS
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LTALPLTLGMVYVVIPIAGVFIALFAIIDLIEVATGKEEPYPLVDESEEPRDLDELEA
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/locus_tag="cg2569"
complement(8387. .8911)
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                                                   TAAATTTTGTGGTCTTTGACTCAAACGGCCAGTTACAACAGGTCCATTTAGACCATCAAG
                                                                                                                     CAACCGTCGCCGCCAAAATTCTCGGACTTAGCGATCACGAAATCGTTAAATCCAACCCT
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5699 GAAATTGAAGCGGGAGCCAACCTGCTCAACGTCGCAAAGAAAG	GGATTCCTTACATTCATCGCC 3397/6 CACGGTCTGCAGGGACTCTAT 4678 [
5639 ACGCCGATTGTTTCGAATTACAAGAAAACCGGACCTGTAAACACTTACGGTTTGGGC 5698		39895 4559
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5339 ATGTTTGCCAGCGGAAAGCTTGGCTCAGGTGTTGCGATCGTCCCCACCAAGGGGCAGCTG 5398	4318	
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3779 ATGGACCATAAGGACCTCGCGCAACGCATCCTGCGCGACACTTGGCGGCGAAGACAACATT	TCGAGGACCCAACTGGGCTGATGGGCGGCATTCATCGCCGTTCGCCTAAAAATCCGCTTA 2
3719 GCTTTTGAACAAACATTCATGTCTGAATATTTTTGTTTCTTCCCGGTTAAGGAGAAATTC	TCTACACCGGCAACCTAAAAATTGACGGAAAAGCGCCCGCGCCCCAAAACCTTGTCGAAG
3659 GTACAAATACTTCGCAAAATCCCTTGATCGGACACAAATAAACAGGTTTAATATTGTTTA 	ATGACCTGGATGGATGCTATTCCGGTGGAGCCGTATTTACTGACGGCACACTTAAACTTT 2
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3539 ACGATAATACAGCCATTGAGATAACTGCAGGTGATGGACAGGTTTCATTCGCTTTTCCGG	ATTCCAGGTTTCCCCTTCGCACCAAAGCGCACCGGCTGGGCTCACACCACCACGCCGTTGA
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3299 GATGGGTGCACTGCCTGACTGTGCCCCGCAAGCTTCATTTGCGCAACCACGCGATCTACC	ATGCCACCATCATCGTTGATGAAGCAGCAGCATCCAAGCTGGAAAACGCTGATCACTAC 2
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3179 AGCTGGATTTCGGCCATGAATTCTACGCACCGCAGGTTGCAGTAAACGGTTCTGATGCCT	
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	/organism="Corynebacterium glutamicum" /mol_type="genomic DNA" /db_xref="taxon:1718" /db_xref="taxon:1718" a 61.8%; Score 3687; DB 6; Length 6911; Similarity 100.0%; Pred. No. 0; Similarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0; Gaps	FT cDS synthetase, FT cDS 55706577 FT cDS phospho-N-acetylmuramoy transferase, Location/Qualifiers 16911	CDS CDS	KOTO, PI MASAKAZ KOTO, PI MATSUI Y C(12N15/09,C12N1/21, randedness: Double; topology: Linear Key Source /stra	PATENTE GENER ORIGINALED FROM CORINBFORM ENCIERIUM AND 115 PATENTE ID 1996196280-A 1 06-AUG-1996; PATINOMOTO CO INC OS Brevibacterium lactofermentum PN JP 1996196280-A/1 PD 06-AUG-1996 PD 06-AUG-1996	accerium glutamicum acterium glutamicum a; Actinobacteria; Actinobacteridae; Actinomyce a; Actinobacteria; Actinobacteridae; Actinomyce acterineae; Corynebacteriaceae; Corynebacterium es 1 to 6911) c,M., Otona,K., Nagase,K., Tsuchiya,M., Matsui, c,M., Otona,K., Nagase,K., Tsuchiya,M., Matsui, ca,Y. and Nakamatsu,W.	
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2401 AATGATCCCAACGGAATGTACGTCGATGGAGATACCCTCCACGTCTACTACCAGCACGAT 2460	2341 CACACAGAACTTTCCAGTTTGCGCCCTGCGTACCATGTGACTCCTCCGCAGGGCAGGCTC 2400	2281 TCTCATGGAGCAATTAAAGCTGCGCTAGAAACAAAAAGGAAAGTACTATGTGTGGGGCTATG 2340	2221 GCCACCATCATCGTTGGATGAAGCAGCAGTATCCAAGCTGGAAAAACGCTGATCACTACCG 2280		2101 CCGCGCGAAAACATCGTGTTGGTGGCAACTGGTGAAGGAAAAAGCCGACGCCATCCGCGG 2160	2041 CTTCAACACCATCGAAGAGGTCCCAACCCACGCGTCACCCAGGGTTTGGGCACTTTGTC 2100	1981 GTCAGGACTGACAAAGGTCCAGGCGCTGCACCCTAAAACTGTGGAGGACAACGCTCGATT 2040			1801 AGTTCACTGACACATCGACATCGTTGATGAAGAGGTCTACAGCCCAGATGGTGCAAACC 1860 		1681 TCATTCGCATGTATGAAGCTGGGGAAGTGTCATTCAAGAACTGCAAGGCATTCTTGGTTGG	1621 ACAAGGGTGGAACCTTGGGGCTTGCAACAGGATCCTCACCACTGAGTACCTACC	1561 TCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGTTGCAGTCCTAATCGCACCCTTCGCCA 1620	1501 TACTTTAAGTACGAGTAAAACTATCCTGATTTTAAAGGAGTCCCACCATGGAAATCACTA 1560 	1441 CARATTITGIGGICTTIGACICARACGGCCAGGIGCARAAGGICCAITTAGGICATCAAG 1500	1381 CAACCGTCGCCGCTAAAATTCTCGGTCTTGGCGATCACGAAATCGCTAAATCCAACCCTG 1440	
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481 CAGCACCTAAAAACGCAGGATTCCACCCCGAACTCCCCACGATTGTTCCCGGTTTTATTG 540	421 GGGTGATTGATGGCTTTCTCCAACTCGAAAACGGCATCATCACGGAACTCTCTGGAGAAC 480	361 ATCAAGAAAATGCAGGTCAAGCAGTTAAAAAAATTGAGGGAAGAATTGTTCCCCCCCTCG 420	301 CGTCCTATGCTTGCTGGAAGGAACCAAATAACCTCAGAAAGATGGCAGAAGTGGTGCATT 360	241 CAACAGCAGGCCTCAAGTCCGAAGATAATTAACCTAGATCCGTAGACATAAGACATCATA 300	181 TCTGCAGTTTTTAAGTTATGCATCATCAGCTTGGAAGGCTGAGGTAATTCAGTAGACCTG 240	121 GAACCCATGGTGTTCCTTGTGGGTTGAGGGAACGAGTGCGGGTGAGAAGTTTTTCAAGTG 180	61 ACGCTCCCGTCGACTGGAGTGGGGTCATTACGGGTGGGATCACGCCGGTGAAAGTTGCG 120	1 AGTCCGTCGACGCCACCATTGATGTGGTGGTCACCGAGCTTGCGGAGGCTTTCTACATCT 60	atch cal Similari 3687; Cons	rce	If I (Dases 1 to 6911) S Tsuchiya,M. and Miwa,K. Sucrase gene derived from coryneform bacteria Li Patent: US 556776-A 4 17-SEP-1996;		Sequence 4 from patent US 5556776. 126124 126124.1 GI:1605994	10010 ha 1200 ha 1200 ha	3661 ACAAATACTTCGCAAAATCCCTTGATC 3687 	3601 CTTCAAAGGTGACACTATTGAGAGATAAGTCATATAAAAGGGTCTTTTGTGGCGAATTGT 3660	3541 GATAATACAGCCATTGAGATAACTGCAGGTGATGGACAGGTTTCATTCGCTTTTCCGGGC 3600
Db &	? B &	S B 8	}	5 B &	? B 9	gb 42	B &	Q B &	Qy db	Оу	Ωy	dg dg	dg VQ	B &	ОУ	Qy Db	dd VQ
1561 TCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGTTGCAGTCCTAATCGCACCCTTCGCCA		THE CANALITITE GENERAL CHARLES CANALITITE CANAL	381	21	1261 ATGGAGTCGCCCGTCTGCGCGATGGCGGCCATCGCCGGGGGCACACACA	21 2	4 1	1081 TTGCTGCGGCACGTGCCGGGGACGCATATGTTGAGTTGA	1021 ATTTGTTCAANGCGANGCCTCCGCTGCATCATAGGGCTCCCGGCAGCGTGGGCGCTTTGC	961 ATACCACTACCAGCGCÁATTGCCTTGGCTAAAGAGAAAAATGTGACGGTCACGGCTACGC	901 TCGATCTCTGCGCAGCGCACCACATCATTGCTTCCTTCGGGCACACTGATGCAGATTTTG	841 GAAAAGGTTGGATCAAATCGATCACAGTAGCGCCGGAAACTGACAATCTTTCTGAGCTTC .	781 AAAACCCGGATTTCATTTTTCCCGGCAACCCAACAGATCTTGCCCGGGTGATCCATGCGG	721 TCCTGCTGTGCGGCATTCACCTCGAGGGCCCTTTCATCAACGCATGCCGTTGTGGTGCTC	661 CGGCGCCGGCTGACGCACTGGCAGCGCAGGTGGAAAACCTTATTCCCTTGTGTGAAGAGG	601 GGAACACCGCGCAGTATCACCGCGAACATGGCACGGTGATGTTTGCCAAGCATGGTTT	541 ATCTTCATAATCACGGTGGAAACGGTGGCGCGTTTCCTACGGGAACGCAGGACCAGGCGA

2641 TACACCGGCAACCTAAAAATTGACGGAAAGCGCCGCGCC	681 TCATTCGCATGTATGAAGCTGGGGAAGTGTCATTCAAGAACTGCAAGGCATTCTTTTGTG. 681 TCATTCGCATGTATAAAGCTGGGGGAAGTGTATCAAAACTGCAAGGCATTCTTTTTGCAAAG 741 ATGAATACCTTGACCACTCTACCCCTGTGACGAAGTGTAAAACAGTCAAAGCCATTCTTTTTTTGGAAAG 801 AGTTCACTCACACTCGACACTCGACACTGTTGAAAACAGTCAAAACCATTCAAAAC 801 AGTTCACTCACAACCACACTCGACACTGTTGAAAACAGTCAAAAACCATTCGCAAAC 801 AGTTCACTCACAAACAACCACACTCGACAACTGTTGAAAACAGTCAAAAACCATTCGCAAAC 801 AGTTCACTCACAAACAACACCGCAAAACAGCCAAAAAACCACTTCAAACCATTCGCAAAC 801 AGTTCACTCACAAAAAAAAAAACACCACACACAACACCACAACA	1621 ACAAGGGTGGAACCTTGGGGCTTGCAACAGGATCCTCACCACTGAGTACCTACC
RESULT 7 BD165105 LOCUS BD165105 DEFINITION Novel polynucleotide. ACCESSION BD165105	DE 2761 GOUGNACCICCOMOGNATICACIONALICATION CONTROLLICATION CON	2701 GAGGACCCAACTGGGCTGATTGGGCGGCATTCATCGCCGTTCAAAAATCCGCCTTATC

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Qy 3959 TTCCAGATCATCGTCGGGCCAGGCGATGTGGATCATGTTTTCAAAGAACTCGATGACGCA 4018	Query Match Best Local Similarity 96.6%; Pred. No. 0; Matches 1915; Conservative 0; Mismatches 68; Indels 0; Gaps 0; Qy 3779 ATGGACCATAAGGACCTCGCGCAACGCATCCTGGCGGCAACACATT 3838	PC C12N15/09,C12N15/09,C07K14/34,C07K16/12,C07K16/40,C12M1/00, PC C12N1/15, PC C12N1/15,C12N1/21,C12N5/10,C12N9/00,C12N9/02,C12P7/40,C12P13/PC C12N13/108, PC C12P19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC G01N33/569,G01N33/569,G01N37/00//C12P21/08,(C12N1/21,C12R1:15), PC G01N33/569,G01N33/68,G01N37/00//C12P21/08,(C12N1/21,C12R1:15), PC C12N1/21,C12R1:13),(C12N1/21,C12R1:01),(C12P13/08,C12R1:15), PC C12N15/00,C12N15/00 PC C12N15/00,C12N15/00 PC C12N5/00,C12N15/00 PC C12N5/00,C12N15/00 CC Novel polynucleotide. FH Key I .1983 FT Source 1 .1983 /organism="unidentified" /mol type="genomic DNA" /mb_xref="taxon:32644" ORIGIN	H •
Oy 1261 GCAGTTGCGTTGGGCGGTAGTTCTTGGGTGTTTCTATGATGCAGTGCCAGATTGCT Oy 5099 GTCATGTTCTTGGTTTGCGCGGTAGTTACCTTTGTCATCGATTCGGCGGAGTGCT Db 1321 GTCATGTTCTTGGTTTGCGCGGTAGTTACCTTTGTCATCGATTCGGCGCAGCGATTGCT Oy 5159 FATGGCCTTTACTTGGTTTGCGCCGCAACGGCAGTCGATTCGCAGTCGCAGCGATTGCT OY 5159 TATGGCCTTTACTTGGTTCGCCGCAACGGCAGCAATTGCATCGCAGCGATTGCT Db 1381 TATGGCCTTTACTTGGTTCGCCGCAACGGCAGCATTGATCCAGACCGCTGCTCCA OY 5219 GTCATGTTCTTGGTTCGCCGCAACGGCAGCATTGATCCAGACCGCTGCTCCA 140 5219 GTCCTGCAGAACGACCAAAGCCGAACGAACGACCGCAGAACTTCC 5278 1441 GTGCCTGCAGGAACGACCAAAGCCGAAAGCACCCGCAGAATTTTCAAACGATTCC 5278 1441 GTGCCTGCAGGAACGACCAAAGCCGAAAGCACCCGCAGAATTTTCAAACGATTCC 5278 1441 GTGCCTGCAGGAACGACCAAAGCCGAAAGCACCCGCAGAATTTTCAAACGATTCC 5278 161111111111111111111111111111111111		Oy 4499 GTCTCTGGATTCTGGCAAGGAAGGTTCCTGCACAGGCGACTCATGGCACTGCA Db 721 GTTTCTTGGATTCTGGCAAGGATCGAGAAGGTTCCTGCACAGGCGACTCATGCA Qy 4559 GACTTCCTGATCACCCCAGTGTTGACTCTGCTCACCGAGAGCGACTCAAGGCACTGCA Qy 4619 ATTGGTCCAGCAATGCGCTGATGCTGACTGACTGCACAGGATTCCTTACGTTCATTCCT Db 841 ATTGGTCCAGCAATGCGCTTGGTGACTTTGCTGCACAGGGTCTCTACAGTCTAT Qy 4679 GATTTCGGTGGTCAGTCGGTGGGTGGTGCTGCACACGGTCTACAGTCTAT Qy 4679 GATTTCGGTGGTCAGTCGGTGGTGGTGTTTTCGGTCTGACACAATCGTTAT Qy 4679 GATTTCGGTGGTCCAGTCGGTGGTCTGCTTTTCGGTCTGGTCTACCAATCGTTATC ATTGGTCCAGCAATGCGCTTGGTCTGCTTTTCGGTCTGGTCTACCAATCGTTATC Qy 4679 GATTTCGGTGGTCCAGTCGGTCTGCTTTTCGGTCTGGTCTACCAATCGTCATC ATTGGTCCAGTCCA	

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3899 GATCGCCAAAGTCTGGATGATGATCCAGATCTGAAAGGCACCTTTGAAACTGGCGGCATG 3958	3839 GTCGCCGCGCACACTGTGCAACGCGTTTACGCCTCGTGCTCAAAGACACCAAGGATGTG 3898	3779 ATGGACCATAAGGACCTCGCGCAACGCATCCTGCGCGGACATTGGCGGCGAAGACAACATT 3838	y Match Local Similarity 96.6%; Pred. No. 0; hes 1915; Conservative 0; Mismatches 68; Indels 0; Gaps 0;	/a /a	Patent: EE		Corynebacterium glutamicum ISM Corynebacterium glutamicum Bacteria; Actinobacteria, Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.	Sequence 2904 from Patent EP1108790. AX122988 AX122988.1 GI:14040476	AX122988	5759 CCA 5761 1981 CCA 1983	5699 GAAATTGAAGCGGGAGCCAACCTGCTCAACGTCGCAAAGAAGAAGCGGTGCCAGCAACA 5758 	5639 ACGCCGATTGTTTCGAATTACAAGAAAACCGGACCTGTAAACACTTACGGTTTGGGC 5698 	5579 GGGGAGCTGCTGTGGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAACC 5638 	5519 GTAAACCTCAACGGCACGCACTTTAACCCGCTGAAGAAGCAGGGGGGATGAAGTCAAAGCA 5578	5459 CGCACTAAGGCTGAGGATGGTTCCAATGTGGATATCTTGATGCACATTGGTTTCGACACC 5518	5399 GTTTCACCAGTGAGCGGAAAGATCGTGGTGGCCCTTCCCATCTGGTCACGCTTTCGCAGTC 5458	5339 ATGTTTGCCAGCGGAAAGCTTGGCTCAGGTGTTGCGATCGTCCCCACCAAGGGGCAGCTG 5398	1501 ACCATCATCCAGGCACCTTTGACCGGTGAAGCTATTGCACTGAGCAGCGTCAGCGATGCC 1560
Db Qy	D Q	B 5) B Q	B &	g Q	ъ Q	g Q	D QV	DB QY	DB QY	B Q	B 8	B &	B 6	g Q	p Q	B &	Db
4979 TACATTGGTATCGGTACCGCACCTATCGGTGCGCTTTGATTGCACTCTTTGATATCAAG 5038	19 GTTCTTGGTATTACAGAGCCTGCGATCTTCGGTGTGAACCTTCGCCTGCGCTGCGCTGCG 	B1 TTCTTCCTGGCGAAGAGTGAAAAGCTCAAGGGCCTTGCAGGTGCTTCAGGTGTCTCCGCT	99 TTCATCTTCGCAACCGCATCCATGGCCAATATCGCGCAGGGTGCAGCATGTTTGGCAGTG	4739 ACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTCAACCAGGGTGGATCC 4798	4679 GATTTCGGTGGTCCAGTCGGCGGTCTGCTTTTCGGTCTGGTCTACTCACCAATCGTTATC 4738	4619 ATTGGTCCAGCAATGCGCTGGGTGGGTGACTTGCTGGCACACGGTCTGCAGGACTCTAT 4678	4559 GACTTCCTGATCACCCCAGTGTTGACTCTGCTGCTCACCGGCTTCCTTACGTTCATTGCT 4618	4499 GTCTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCATGGGCACTGCA 4558	4439 CTGTTTGGTTTGGATGTTGCTCAAGCTGGTTACCAGGGCACCGTGCTTCCTGTGCTGGTG 4498	4379 CTGGTTAACGGCTACGACGTGGCCGCCACCATGACCGCGGGGGGAAATGCCAATGTGGTCC 4438	4319 CGTTTCGGTGGCAATGAGTTCCTGGGCGCCGGCATTGGTATGGCGATGGTGTTCCCCAACC 4378	4259 CTGATGGCATCTGCGCGTTCGCGTTCTGCCAGTGTTGGTTTGACCGCAACCAAG 4318	4199 GGTCCGCAATCACTGGTGGAGATGTTCCCTCAGATCAGCGGTGTTGCTGAGATGATCAAC 4258	4139 TTGGTTGGTGGCGGTCTGCTCATGGCTATCAACAATGTGTTGGTTG	4079 AACTGGTTCAGCCGTGCTGTGAAGGTATTGGCGGACATTTTCGTCCCGCTGATTCCAATC 4138	4019 ACCTCCAAAGACATCGCTGTGTCCACAGAGCAGCTCAAAGATGTTGTGGCTAACAACGCC 4078	3959 TTCCAGATCATCGTCGGGCCAGGCGATGTGGATCATGTTTTCAAAGAACTCGATGACGCA 4018	121 GATCGCCAAAGTCTGGATGATGATCCAGATCTGAAAGGCACGTTTGAAACGGGTGGTATG 180

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Corynebacterium thermoaminogenes
Corynebacterium thermoaminogenes
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 1656), Matsuzaki,Y., Akiyoshi,N., Nakamura,K., Hirano,S., Nomaka,G., Matsuzaki,Y., Akiyoshi,N., Nakamura,K., Kimura,E., Osumi,T., Matsui,K., Kawahara,Y., Kurahashi,O., Nakamatsu,T. and Sugimoto,S. Genes for heat resistant enzymes of amino acid biosynthetic pathway derived from thermophilic coryneform bacteria Patent: WO 0125447-A 71 12-APR-2001;
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OS COTYNEBACTETIUM THETMOAMINOGENES
PN WO 0125447-A/71
PD 12-APR-2001
PP 04-OCT-2000 WO 2000JP006913
PF 04-OCT-1999 JP 99P 282716,01-NOV-1999 JP 99P 311147 PR 21-APR-2000 JP 09P 282716,01-NOV-1999 JP 99P 311147 PR 21-APR-2000 JP 00P 120687
PI SEIKO HIRANO, GEN NONAKA, YUMI MATSUZAKI, NAOKI AKIYOSHI, KANAE PI BITCHIRO KIMURA, TSUYOSHI OSUMI, KAZUHIKO MATSUI, YOSHIO KAWAHARA, PI BITCHIRO KIMURA, TSUYOSHI NAKAMATSU, SHINICHI SUGIMOTO PC C12N9/12, OSAMU KURAHASHI, TSUYOSHI NAKAMATSU, SHINICHI SUGIMOTO PC C12N9/12, C12N15/54, C12N15/53, C12N15/31, C12N15/56, C12N9/88, PC C12N9/04, C07K14/34, C12N9/26, C12N3/04
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                                                                                               ATGCATCCTATGACCTGGATGGATGCTATTCCGGTGGAGCCGTATTTACTGACGGCACAC
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/mol_type="genomic DNA"
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TGGCGAATTGTACAAATACTTCGCAAAATCCCTTGAT 3686 	CTTTTCCGGGCCTTCAAAGGTGACACTATTGAGAGAGATAAGTCATATAAAAGGGTCTTTTG 3649	TGATCGCGGACGATAATACAGCCATTGAGATAACTGCAGGTGATGGACAGGTTTCATTCG 3589	GTTIGICTGIGGATCGIGATCGICATCGCGIAGCIGAGGIAAAACCIGGCGAATTAG 3529 	GTTCTGAACCTGTCCGAGTAGACATCCGAGGCAATATTTCCCTCGAGTGGGATGGTGTCC 3469 -	CGATCTACCAAGAGCTCCTTCTCCCAGAGGGGGGAGTCGGGGGGTAATCAGATCTGTATTAG 3409 	CACAGGAAGGATGGGTGCACTGCCTGACTGTGCCCCGCAAGCTTCATTTGCGCAACCACG 3349 	CTGATGCCTGGCTCGTGGGCTGGATGGGGCTGCCCCCGCGCAGGATGATCACCCAACAGTTG 3289	GATTCAGCGAGCTGGATTTCGGCCATGAATTCTACGCACCGCAGGTTGCAGTAAACGGTT 3229 	CTGACCAGTGCGGATATGTCGTCGACAAGCTTGAAGGAACGACCTTCCGCGTCTTGCGAG 3169	TGATTTTCTGTCCACAAGGATTGGACCGAATCCACGATGAGGTTACTCACTACGCAAGCT 3109	GGGAATGCCCCAACCTTTTTACGCTTCGCGATGAAGAAACTGGCGAAGATCTCGACGTGC 3049 	TTGACCTCAGTGATGCACAACCTGGTTCTGCTCCTGATCTCGTTCCCGATGGCTACATGT 2989	CAGCGGTTCTATACCGCTCGACAGATCTTGAAAACTGGGAATTCTCCCGGTGAAATCACCT 2929	GCCCTGATGGTGGTTGGAACATGGTTCTTGGGGCCCAACGCGAAAACCTCACCGGTG 2869 	ATCCGCTTATCGACGGACCCGCCAGCGGTTTCACACCCCATTACCGCGATCCCATGATCA 2809	TTGTCGAAGTCGAGGACCCAACTGGGCTGATGGGCGGCATTCATCGCCGTTCGCCTAAAA 2749 	

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AX069134
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                  CATTGGCCCAGCAATGCGCTGGGTGGGCGCATGTGCTGGCACACGGTCTACAGGGACTTTA
                                                                                                                                          AGACTTCCTGATCACCCCAGTGTTGACTCTGCTGCTCACCGGCTTCCTTACGTTCATTGC
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TGATTTCGGTGGTCCAGTCGGCGGTCTGCTTTTCGGTCTGGTCTACTCACCAATCGTTAT
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                                                                                                                      AGACTTCCTGATCACTCCAGTGCTGACGTTGCTGCTCACCGGATTCCTTACATTCATCGC
                                                                                                                                                                                               GGTTTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCAAGGGCACTGC
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/db_xref="taxon:1718"
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                                                     ACCATAAGTTGAAACCTTGAGTGTTCG
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Score 1412.6; Pred. No. 0; 0; Mismatches

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Genes of corynebacterium Patent: WO 02051231-A 9 04-JUL-2002; BASF AKTIENGESELLSCHAFT (DE)
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Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                          Pompejus, M., Kroeger, B., Zelder, O. and Genes of corynebacterium
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/mol_type="unassigned
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                                                                                                                                                                                                                            organism="Corynebacterium"
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                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                   note="unnamed protein
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from Patent WO02051231.
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1501 ACCATAAGTTGAAACCTTGAGTGTTCG	5758 ACCATAAGTTGAAACCTTGAGT	1441 CGAAATTGAAGCGGGAGCCAAC	5698 CGAAATTGAAGCGGGAGCCAAC	1381 CACGCCGATTGTTTTCGAAT	5638 CACGCCGATTGTTTGTTTCGAAT	321	5578 AGGGGAGCTGCTGTGAATTC	5518 CGTAAACCTCAACGGCACGCAC	201	5458 CCGCACTAAGGCTGAGGATGGT	1141 AGTTTCTCCGGTGAGTGGAAAG	5398 GGTTTÇAÇÇAGTGAGCGGAAAG	081	338	1021 CACCATCATCCAGGCACCTTTG	961	18	5158 TTATGGCCTTTACTTGGTTCGC	5098 GGTCATGTTCTTGGTTTGCGCC 	038 781	721	78	4918 TGTTCTTGGTATTACAGAGCCT	4858 GTTCTTCCTAGCGAAGAGTGAA 	4798 CTTCATCTTCGCAACCGCATCC	4738 CACTGGTCTGCACCAGTCCTTC	17.5
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BASF AKTIENGESELLSCHAFT (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Corynebacteriaceae, Corynebacterium.
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             /note="unnamed protein product; RXA00041"

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AATTGACGGAAAGCGCCGCCGCCACCCAAAAACCTTGTCGAAGTCGAGGACCCAACTGGGCT 2717

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Patent: JP 2002191370-A 2905 09-JUL-2002;
RYOWA HAKKO KOGYO CO LTD
OS COTYNEDSACTETIUM Glutamicum
PN JP 2002191370-A/2905
PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI 15-DEC-2000 JP 2000405091
PSATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEII
PI KEIKO OCHIAI,
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Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K., Yokoi, H., Tateishi, N., Senoo, A., Ikeda, M. and Ozaki, A.
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/db_xref="taxon:32644"
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RESULT 14 AXI12989 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	B &	B 8	B 8	B &	B 8	B &	B 8	g Sy	g Q	в Q	g Qy	g Qy	40 40
AX122989 AX122989 N Sequence 2905 from Patent EP1108790. AX122989 AX122989.1 GI:14040477 Corynebacterium glutamicum Corynebacterium glutamicum Bacteria; Actinobacteria, Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium. Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K., Yokoi,H., Tateishi,N., Senoh,A., Ikeda,M. and Ozaki,A. Novel polynucleotides Patent: EP 1108790-A 2905 20-JUN-2001; KYOWA HAKKO KOGYO CO., LTD. (JP)	3587 TCGCTTTTCCGGGCCTTCAAAGGTGACACTATTGAGAGA 3625 	3527 TAGTGATCGCGGACGATAATACAGCCATTGAGATAACTGCAGGTGATGGACAGGTTTCAT 3586	3467 TCCGTTTGTCTGTGGATCGTGATGGTGATCGTCGCGTAGCTGAGGTAAAACCTGGCGAAT 3526	3407 TAĞGTTCTGAACCTGTCCGAGTAGACATCCGAGGCAATATTTCCCCTCGAGTGGGATGGTG 3466 	3347 ACGCGATCTACCAAGAGCTCCTTCTCCCAGAGGGGGAGTCGGGGGTAATCAGATCTGTAT 3406 	3287 TTGCACAGGAAGGATGGGTGCACTGCCTGACTGTGCCCCGCAAGCTTCATTTGCGCAACC 3346	3227 GTTCTGATGCCTGGCTCGTGGGCTGGATGGGGCTGCCCGCGCAGGATGATCACCCAACAG 3286	3167 GAGGATTCAGCGAGCTGGATTTCGGCCATGAATTCTACGCACCGCAGGTTGCAGTAAACG 3226 	3107 GCTCTGACCAGTGCGGATATGTCGTCGACAAGCTTGAAGGAACGACCTTCCGCGTCTTGC 3166 	3047 TGCTGATTTTCTGTCCACAAGGATTGGACCGAATCCACGATGAGGTTACTCACTACGCAA 3106	2987 TGTGGGAATGCCCCAACCTTTTACGCTTCGCGATGAAGAACTGGCGAAGATCTCGACG 3046	2927 CCTTTGACCTCAGTGATGCACAACCTGGTTCTGCTCCTGATCTCGTTCCCGATGGCTACA 2986	
													
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Qy 1262 TGGAGTCGCCCGTCTGCGCGATGGCGGCGCCATCGCCGGGGGCACCATAGCGAG 1321		OHALDICON CONTROL OF THE CONTROL OF THE CANCEL OF THE CANC	722 481 782 541 842 601	301 TCTTCATAATCACGGTGGAAACGTGGCACGGAACGGAAC	Db 61 GTCCTATGCTTGCTGAAGGAAGCAATAACCTCAGAAAGAA

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ALIGNMENTS

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ID AAF3
Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding
                                                                               WPI; 2001-138150/14.
P-PSDB; AAB69080.
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20-APR-2001
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Query Match
Best Local Similarity
Matches 5969; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes the Brevibacterium lactofermentum sucrose PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate-sugar transport system) enzyme II, which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved amino-acid and nucleic acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved amino-acid and nucleic acid productivity. (Updated on 11-SEP-2003 to standardise OS field)
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3901 TCGCCAAAGTCTGGATGATGATGATCAGAATCTGAAAAGGCACCTTTGAAACTGGCCGCATGTTTGATGATGATGATGATGATGATGATGATGATGATG	Qy 3721 TTTTGAACAAACATTCATGTCTGAATATTTTTGTTTCTTCCCGGTTAAGGAGAAATTCAT 3780 Db 3721 TTTTGAACAAACATTCATGTCTGAATATTTTTTGTTTCTTCCCGGTTAAGGAGAAATTCAT 3780 Db 3721 TTTTGAACAAACATTCATGTCTGAATATTTTTTTTTTTCTTCCCGGTTAAGGAGAAATTCAT 3780 Qy 3781 GGACCATAAGGACCTCGGGCAACGCATCCTGCGCGACATTGGCGGCGAAGACATTGT 3840 Db 3781 GGACCATAAGGACCTCGGCGCAACGCATCCTGCGCGACATTGGCGGCGAAGACACATTGT 3840 Db 3841 CGCCGCCACACTGTGCAACGCGTTTACGCCTCCTGCAAAGACACCCAAGGATGTGGA 3900 3841 CGCCGCCGCACACTGTGCAACGCGTTTACGCCTCCTGCTCAAAGACACCCAAGGATGTGGA 3900 Db 3841 CGCCGCCGCACACTGTGCAACGCGTTTTACGCCTCCTGCTCAAAGACACCCAAGGATGTGGA 3900		3421 GTCCGAGTAGACATCCGAGGCAATATTTCCCTCGAGTGGGATGGTGTCCGTTTGTCTCTGTG 3421 GTCCGAGTAGACATCCGAGGCAATATTTCCCTCGAGTGGGATGGTGTCCGTTTGTCTCTGTG 3421 GTCCGAGTAGACATCCGAGGCAATATTTCCCTCGAGTGGGATGGTGTCCGTTTGTCTTGTC 3421 GTCCGAGTAGACATCCGAGGCAATATTTCCCTCGAGTGGGAATGATTAGTGATCGCGGAGTAGTGATCGTCGGGTAAAACCTGGCGAATTAGTGATCGTCGAGTGAGT	نا نا نا نا نا	3061 CACAAGGATTGGACCGAATCCACGATGAGGTTACTCACCAACGGTTCTGACGAAGGA 3121 GGATATGTCGTCGACGAAGCTTGAAGGAACCCTTCCACGTCTTGCGAGGATTCAGCGAG 3121 GGATATGTCGTCGACGAAGCTTGAAGGAACCCTTCCGCGTCTTGCGAGGATTCAGCGAG [Qy 3001 AACCITTTACGCITCGCGATGAAGAAACTGGCGAAGATCTCGACGTGCTGATTTTCTGT 3060

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AC AAH68533;
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DT 26-SEP-2001 (first entry)
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DE C glutamicum coding sequence fragment SEQ ID NO: 7068.
XX
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Coryneform bacterium; amino acid synthesis; vitamin; saccharide KW organic acid synthesis; ds.
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OS Corynebacterium glutamicum.
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PN EP1108790-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
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07-APR-2000; 2000JP-00159162.
03-AUG-2000; 2000JP-00280988.
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                         ATCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGTTGCAGTCCTAATCGCACCCTTCGCC
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                                                                                                                                                              CAAATTTTGTGGTCTTTGACTCAAACGGCCAGGTGCAAAAGGTCCATTTAGGTCATCAAG 1500
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                                                                                                                                                                                                                                  CAACCGTCGCCGTAAAATTCTCGGTCTTGGCGATCACGAAATCGCTAAATCCAACCCTG
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5939 GCAGTAGCGTTTGATATTTTGCGCCGCTG 5967 	5879 TCGGTGTACCTGTGTGGTGCCACCCCGCAATCTTCACCCCACATTGGACATGTTCGTTC	ATCTTTGACACCGGTACCCGTACGCTTCGAGATTTTAAACCTGTTCAACCAGGTCATGCC	CCATAACTTGAAACCTTGAGTGTTCGCACACAGGTTAGACTAGGGGACGTGACTCTACGC	5699 GAAATTGAAGCGGGAGCCAACCTGCTCAACGTCGCAAAGAAAG	5639 ACGCCGATTGTTTCGAATTACAAGAAAACCGGACCTGTAAACACTTACGGTTTGGGC 5698 	GGGAGCTGCTGTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAACCCGTTATGAGGTTATGAGGTAACCCGTGTGTGAAGTTGATGCCATTAAGGCTGCAGGTTATGAGGTAACCCGGGAGGTTATGAGGTAACCCGGAGGTTAAGGCTGCAGGTTAAGGCTGCAGGTTAACGCGAGGTAACC	GTAAACCTCAACGGCACGCACTTAACCCGCTGAAGAACCAGGGCGATGAAGTCAAAGCA	GGACTAAGGCTGAGGATGGTTCCAATGTGGATTATCTTGATGCACATTGGTTTCGACACT	GTTTCACCAGTGACGGAAAGATCGTGGTGGCCTTCCCATCTGGTCACGCTTTCGCAGTC	ATGTTTGCCAGCGGAAAGCTTGGCTCAGGTGTTGCGATCGTCCCCACCAAGGGCAGCGCTTGCTT	ACCATCATCCAGGCACTTTGACCGGTGAAGCTATCGCACTGAGCAGCGCTCAGCGATGCC	5219 GTGCCTGCAGGAACGACCAAAGCCGAAGCAGAAGCACCCGCAGAATTTTCAAACGATTCC 5278	5159 TATIGGCCTTTACTTCGCTCCCCCAACGCAGCAGTTCATCCAGATGCAACCGCTGCTCCA 5218	GTCATGTTCTTGGTTTGCGCGGTAGTTACCTTTGTCATCGCATTCGGGCGAGCGA	GCAGTTGCGTTGGGCGCTGCCAGGTTTCTTGGGTGTTCTATTGATGCTCCAGATATG			110726 TTCTTCCTGGCGAAGAGTGAAAAGCTCAAGGGCCTTGCAGGTGCTTCAGGTGTCTCCGCT 11066

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           A DNA fragment (AAT34177) includes an open reading frame (ORF-F2) coding for sucrase. It was obtd. by screening a genomic library of Brevibacterium lactofermentum ATCC 13869 with probes (see also AAT34178-80) based on homologous regions of known sucrase, levanase and invertase genes. An isolated fragment was inserted into pSAC4, giving plasmid pSSM30. Escherichia coli JM109/pSSM30 was named AJI3047 and deposited as FERM BP-4800. Over-expression of the sucrase gene in a coryneform bacterium improves the ability of the host to assimilate sucrose, resulting in increased fermentation rates and improved productivity of L-amino acids (esp. L-lysine and L-glutamic acid) and nucleic acids from raw materials contg. sucrose. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugimoto
Yasuhiko
                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                          Sucrase gene from Coryneform bacteria - used of microorganisms for improved prodn. of L-amino
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N-acetylmuramoylalanyl-D-glutamyl- meso-6-diaminopimelate
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                      <u>АТАССАСТАССАGСGСААТТGССТТGGСТАААGAGAAAAATGTGACGGTCACGGCTACGC</u>
                                                                                                            TCGATCTCTGCGCAGCGCACCACATCATTGCTTCCTTCGGGCACACTGATGCAGATTTTG
                                                                                                                                                       GAAAAGGTTGGATCAAATCGATCACAGTAGCGCCGGAAACTGACAATCT
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61.8%; So ilarity 100.0%; F Conservative 0;
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                          Nakagawa
Tateishi
  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coryneform bacterium; organic acid synthesis
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Best Local Similarity
Matches 1915; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly I-lysine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1983 BP; 410 A; 508 C; 558 G; 507 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2904; 246pp + Sequence Listing; English
                                                                      GGTCCGCAATCACTGGTGGAGATGTTCCCTCAGATCAGCGGTGTTGCTGAGATGATCAAC
                                                                                                                                  TIGGITGGIGGCGGICIGCICATGGCTATCAACAAIGIGTIGGTIGGCGCAGGAICIGTIC
                                                                                                                                                                              AACTGGTTCAGCCGTGCTGTGAAGGTATTGGCGGACATTTTCGTCCCGCTGATTCCAATC
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     CTGATGGCATCTGCGCCGTTCGCGGTTCTTGCCAGTGTTGGTTTGGTTTCACCGCAACCAAG
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                       GGGGAGCTGCTGTGTAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAACC
                                                                                                                                                                                                                                                                                                                                                                                           ATGTTTGCCAGCGGAAAGCTTGGCTCAGGTGTTGCGATCGTCCCCACCAAGGGGCAGCTG 5398
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                                                                                                                  GTAAACCTCAACGGCACGCACTTTAACCCGCTGAAGAAGCAGGGCGATGAAGTCAAAGCA
                                                                                                                                                                            CGCACCAAGGCTGAGGATGCTTCCAATGTGGATATCTTGATGCACACTTGGTTTCGACACA
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2031 ACGCTCGATTCTTCAACACCATCGAAGAGGTCCCAACCCACGCCGTCACCCAGGGTTTGG

Query Match
Best Local Similarity
Matches 1545; Conserv

Conservative

Score 1457; DI Pred. No. 0; 0; Mismatches

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Length 0 Other;

Sequence

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392 A; 456 C; 24.4%;

432 G; 376

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01-NOV-1999;
21-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hirano S,
Kimura E,
                                                                       The present sequence is provided in a specification relating to genes encoding thermophilic amino acid biosynthesis system enzymes of the thermotolerant bacterium Corynebacterium thermoaminogenes. The novel proteins retain at least 30% isocitrate ligase activity after heating at 500C for 5 minutes. DNA fragments encoding the enzymes were isolated from a Corynebacterium thermoaminogenes chromosomal DNA plasmid library by PCR. The DNA may be used for developing strains of amino acid producing
                                                                                                                                                                                                                                                                                                                                                      Proteins
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-300170/31.
P-PSDB; AAB83190.
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Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as marker

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ABS65346 standard; DNA; 1527

15-NOV-2002 (first entry)

DNA encoding : glutamicum metabolic pathway (MP) protein

RRSULT 7
ABS653A
XX ABS66
XX ABS6
XX ABS6
XX DNA
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XX Meta
COfa
XX Orga
X Metabolic pathway protein; MP; cell metabolism; amino acid; vitamin; cofactor; nucleotide; nucleoside; trehalose; fine chemical production; organic acid; non-proteinogenic amino acid; purine base; carbohydrate; pyrimidine base; lipid; unaaturated fatty acid; diols; polyketide; aromatic compound; food industry; animal feed; cosmetic industry; pharmaceutical industry; gene; ds.

Corynebacterium glutamicum ATCC 13032

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Best Local Simi
Matches 1462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of Corynebacterium glutamicum metabolic pathway (MP) proteins, and the polymucleotide sequences encoding them. The MP proteins are enzymes involved in the metabolism of molecules important for the normal functioning of cells (e.g. amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose). The polymucleotide sequences encoding the MP proteins are useful for producing fine chemicals, particularly organic acids, non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, (un)saturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes. The fine chemicals are useful in the food, animal feed, cosmetic or pharmaceutical industries. ABS65342-ABS65364 encode the C. glutamicum MP
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 metabolism and oxidative to AAB 79633 which are ir production. The C. glutam
                                                                                                                        New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes.
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                                                     AAF71360 to AAF71750 encode the Corynebacterium glutamicum
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3-SEP-1999;
3-SEP-1999;
3-SEP-1999;
3-SEP-1999;
3-SEP-1999;
                                                                                                                                                                                                                     2001-061975/07.
DB; AAB79416.
118m and oxidative phosphorylation (SMP) proteins given in 79633 which are involved in carbon metabolism and energy tion. The C. glutamicum SMP gene can be used in carbon metabolism and energy
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                                                                                                                                                                                                                                                                       Kroeger
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cc expression in host cells and production or modulation of production of cf fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a cc nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, ca diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a colyketide, or an enzyme. The presence of (I) or SMP proteins (III) cc encoded by them are used for diagnosing the presence or activity of cc corynebacterium diphtheriae in a subject. (I), (III) or host cells corynebacterium diphtheriae in a subject. (I), (III) or host cells corynebacterium diphtheriae in a subject. (I), (III) or host cells containing them are used to map genomes of organisms related to C. cc glutamicum, identify and localise C. glutamicum sequences of interest, in cevolutionary studies, in determining SMP protein regions required for metabolism of sugars, and in modulating the metabolism of sugars, and in modulating high-energy molecule production of containing supported to contain a cell (i.e. ATP, NADPH)
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P-PSDB; AAG92651.
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07-APR-2000;
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.

SEQ ID NO 2905; 246pp + Sequence Listing; English

the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lygine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing

Sequence 1299 BP; 287 A; 363 C; 350 G; 299 T; 0 U; 0 Other;

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TGTGGGAATGCCCCAACCTTTTACGCTTCGCGATGAAGAAACTGGCGAAGATCTCGACG 	CCTTTGACCTCAGTGATGCACAACCTGGTTCTGCTCCTGATCTCGTTCCCGATGGCTACA	GTGCAGCGGTTCTATACCGCTCGACAGATCTTGAAAACTGGGAATTCTCCGGTGAAATCA 	TCAGCCCTGATGGTGATGGTTGGAACATGGTTCTTGGGGCCCAACGCGAAAACCTCACCG	AAAATCCGCTTATCGACGGACCCGCCAGCGGTTTCACACCCCATTACCGCGATCCCATGA	ACCTTGTCGAAGTCGAGGACCCAACTGGGCTGATGGGCGGCATTCATCGCCGTTCGCCTA	CACTTAAACTTTTCTACACCGGCAACCTAAAAATTGACGGAAAGCGCCGCGCCACCCAAA 	CGGATGCATCCTATGACCTGGATGGATGCTATTCCGGTGGAGCCGTATTTACTGACGGCA	CCACGCCGTTGACCGGACCGCAGCGATTGCAGTGGACGCACCTGCCCGACGCTCTTTACC	ACTACCAGCACGATCCAGGTTTCCCCTTCGCACCAAAGCGCACCGGCTGGGCTCACACCA	CGCAGGGCAGGCTCAATGATCCCAACGGAATGTACGTCGATGGAGAGATACCCTCCACGTCT	TGTGTGGGGCTATGCACACAGAACTTTCCAGTTTGCGCCCTGCGTACCATGTGACTCCTC	0; Mismatches
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                                                                                                                                                                                     New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes.
                                                                                                                                                                      Claim 3;
                                                                                                                                                                                                                                                    Pompejus
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                                                                                                                                                    to AAF71750 encode the Corynebacterium
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و
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or
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CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
CC to AAB 79633 which are involved in carbon metabolism and energy
CC production. The C glutamicum SMP gene can be used in vectors (II) for
CC expression in host cells and production or modulation of production of
CC fine chemicals, such as, an organic acid, a proteinogenic or
CC comproteinogenic amino acid (preferred), a purine or pyrimidine base, a
CC condition of a romatic compound, a vitamin, a cofactor, a
CC diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
CC encoded by them are used for diagnosing the presence or activity of
CC cortaining them are used for map genomes of organisms related to C.
CC glutamicum, identify and localise C. glutamicum sequences of interest, in
CC evolutionary studies, in Metermining SMP protein regions required for
CC function, in modulating SMP protein activity, in modulating the
CC metabolism of sugars, and in modulating high-energy molecule production
CC in a cell (i.e. ATP, NADPH) sugar ven in AAB79243

Sequence 1287 BP; 325 A; 349 Ç 326 G; 287 T; 0 U; 0 Other;

В Ş 뮹 S Query Match Best Local Similarity Matches 1256; Conserv 302 242 61 GTCCTATGCTTGCTGGAAGGAACCAAATAACCTCAGAAAGATGGCAGAAGTGGTGCATTA 361 GTCCTATGCTTGCTGGAAGGAAGCAAATAACCTCAGAAAGATGGCAGAAGTGGTGCATTA Conservative 20.7%; 97.6%; 0, Score 1237.4; Pred. No. 0; 0; Mismatches DB 31; 4; Length 0, Gaps 120 60 301 0

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                                      AACCGTCGCCGAAAATTCTCGGACTTAGCGATCACGAAATCGTTAAATCCAACCCTGT
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WPI; 2001-061975/07. P-PSDB; AAB79449.

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Schroeder H,

Zelder Ó

Haberhauer

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New isolated Corynebacterium glutamicum nucleic acid encoding a sugar

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CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243 CC to AAB 79633 which are involved in carbon metabolism and energy CC production. The C glutamicum SMP gene can be used in vectors (II) for CC expression in host cells and production or modulation of production of CC fine chemicals, such as, an organic acid, a proteinogenic or conproteinogenic amino acid (preferred), a purine or pyrimidine base, a cC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a cC of containing them are used for diagnosing the presence or activity of CC containing them are used for diagnosing the presence or activity of CC containing them are used to map genomes of organisms related to C. CC glutamicum, identify and localise C glutamicum sequences of interest, in CC evolutionary studies, in determining SMP protein regions required for CC unction, in modulating SMP protein activity, in modulating the CC metabolism of sugars, and in modulating high-energy molecule production or a cell (i.e. ATP, NADPH)
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16-DEC-1999; 07-APR-2000; 03-AUG-2000; Coryneform bacterium; amino acid organic acid synthesis; ds. Corynebacterium glutamicum. 26-SEP-2001 AAH67872 standard; 18-DEC-2000; 2000EP-00127688 20-JUN-2001. AAH67872; (КУОМ) КУОМА НАККО КОСУО КК glutamicum 99JP-00377484. 2000JP-00159162. 2000JP-00280988. coding sequence (first DNA; 1152 entry) fragment SEQ ID NO: 뫈 synthesis; vitamin; saccharide;

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Senoh A,
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Ikeda M,
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Ozaki A;
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Pred. No. 1.7e-305;
D; Mismatches 37;
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5516 ACCGTAAACCTCAACGGCACGGACTTTAACCCGCTGAAGAAGCAGGCGATGAAGTCAAA
1081 ACACCATAAGTTGAAACCTTGAGTGTTCG
                                                                                                                                                                             ACCACGCCGATTGTTGTTTCGAATTACAAGAAAACCCGGACCTGTAAACACTTACGGTTTG
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SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purime base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
                                                                                                                                                                                                                                                         Corynebacterium glutamicum SMP protein nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production. The C. glutamicum SMP gene can be used in vectors (II) for expression in host cells and production or modulation of production of fine chemicals, such as, an organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a concleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a copolyketide, or an enzyme. The presence of (I) or SMP proteins (III) concled by them are used for diagnosing the presence or activity of corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells containing them are used to map genomes of organisms related to C. glutamicum, identify and localise C. glutamicum sequences of interest, in evolutionary studies, in determining SMP protein regions required for function, in modulating SMP protein activity, in modulating the metabolism of sugars, and in modulating high-energy molecule production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 751-752; 1246pp; English
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                                                   CGTGGGATTAACGCGCGACGATGAAAACAGCTACTTCAAAACCATTCGTAAAGAGTTCAC
                                                                      CGTGGGACTAACCCGTGACGATGAAAACCAGCTACTTTAAAACCATTCGCAAAGAGTTCAC
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99DE-01042123.
99DE-01042125.
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Senoh A,
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2000JP-00159162.
2000JP-00280988.
                                                                                                                                                                                                                                                                               synthesis;
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da M,
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Novel polynuclectides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene

A gene, and fring homologous :

gene

Claim 8; SEQ ID NO 2906; 246pp + Sequence Listing; English

XSSSSSSSSSSSSXXX

Query Match Best Local Simi Matches 711; The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteriam are useful for producing amino particularly L-lysine. The present sequence is a nucleic acide described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office Sequence 759 BP; 211 A; 209 C; 189 G; 150 T; 0 U; 0 Other; 2267 2147 1848 1728 1548 ATGGAAATCACTATCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGTTGCAGTCCTAATC 1607 2207 2087 2027 1967 1908 1788 1668 1608 601 541 481 421 361 301 241 181 661 121 721 61 μ Similarity GCACCCTTCGCCAACAAGGGTGGAACCTTGGGGCTTGCAACAGGATCCTCACCACTGAGT 1667 GCTGATCACCGTCTCATGGAGCAATTAAAGCTGCGC GCTGATCACTACCGTCTCATGGAGCAATTAAAGCTGCGC CAGATGCACAACAATGCCACCATCATCGTTGATGAAGCAGCAGCATCCAAGCTGGAAAAC TAGATGCACAACATGCCACCATCATCGTTGGATGAAGCAGCAGTATCCAAGCTGGAAAAC 2266 GACGCCATCCGCGGAACTGTGGAAGGCCCACTGACCGCCATGTGCCCAGGTTCCATCCTG GACGCCATCCGCGGAACTGTGGAAGGCCCAGTGACTGCTTCTTGCCCAGGTTCCATCCTG TTGGGCACTTTGTCCCGCGCAAAACATCGTGTTGGTGGCAACTGGTGAAGGAAAAGCC TTGGGCACTTTGTCCCGCGCGCAAAACATCGTGTTGGTGGCAACTGGTGAAGGGAAAAGCC GACAACGCTCGATTCTTCAACACCATCGAAGAGGTCCCAACCCACGCCCTCACCCAGGGT GACAACGCTCGATTCTTCAACACCATCGAAGAGGTCCCAACCCCACGCCGTCACCCAGGGT CCATCATCTTCTCTCTGAGACTGACAAAGGTCCAGGCGCTGCACCCTAAAACTGTGGAG CCATCATCTTCTCTGTCAGGACTGACAAAGGTCCAGGCGCTGCACCCTAAAACTGTGGAG GAATCCGTTGATGTTCAAATCCTTGGCATCGGCGGAAACGGCCACATCGCTTTCAATGAG GAATCCGTTGAAGTTCAAATCCTTGGCATCGGCGGAAACGG-CACATCGCTTTCATTGAA 1966 GATGGTGCAAACCCTGATCCATACGAAGCAGCTGCAGAGTATGAGGCAAAGATCGCTGCA GATGGTGCAAACCCTGATCCCATACGAAGCAGCTGCAGAGTATGAGGCAAAGATCGCTGCA 1907 ACCATTCGTAAAGAGTTCACTGACCACATCGACATCGTTGATGAAGAGGTCTACAGCCCA ACCATTCGCAAAGAGTTCACTGACCACATCGACATCGTTGATGAAGAGGTCTACAGCCCA 1847 GCATTCTTGTTGGATGAATACGTGGGATTAACGCGCGACGATGAAAACAGCTACTTCAAA GCATTCTTGTTGGATGAATACGTGGGACTAACCCCGTGACGATGAAAACAGCTACTTTAAA 1787 ACCTACCAAGAGCTCATTCGCATGTATGAAGCTGGGGGAAGTGTCATTCAAGAACTGCAAG 1727 GCACCCTTCGCAACTAAGGGCGGAACCTTGGGGGCTTGCAACTGGATCGTCACCTTTGAGC ATGGACATCATCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGCGGCAGCCCTGATC ACCTACCAAGAGCTCATTCGCATGTATGAAGCTGGGGAAGTGTCATTCAAGAACTGCAAG Conservative 11.3%; 0, Score 671.8; DB 5; Pred. No. 2.4e-191; 0; Mismatches 47; 759 2305 Indels Length 759; 1; Gaps 2146 2086 360 2206 600 540 2026 420 300 240 660 480 60

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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10357.302 Million cell updates/sec
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US-09-583-110-463
US-09-583-110-463
US-09-107-433-647
US-09-108-001-127
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Sequence 4, Appli
Sequence 3464, Ap
Sequence 5847, Ap
Sequence 5847, Ap
Sequence 56, Appli
Sequence 297, App
Sequence 201, Appli
Sequence 201, Appli
Sequence 1806, Appli
Sequence 1806, Appli
Sequence 1807, Appli
Sequence 1277, Appli
Sequence 2847, Appli
Sequence 2566, Appli
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Sequence 1041, Appli
Sequence 17, Appli
Sequence 2317, Appli
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                                          Query Match
Best Local Similarity
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US-09-107-433-202 US-09-134-000C-1201	US-08-781-986A-1317	US-08-956-171E-1317	US-09-107-532A-1876	US-09-103-840A-1	US-09-103-840A-2	US-09-543-681A-1005	US-09-270-767-15150	US-09-583-110-829	US-09-643-990A-1	US-09-557-884-1	US-09-367-293-1	US-09-221-017B-736	US-09-107-532A-1634	US-08-673-190A-3	US-09-543-681A-984
Sequence 202, App Sequence 1201, Ap	Sequence 231, App		Sequence 1876, Ap	Sequence 1, Appli	Sequence 2, Appli	Sequence 1005, Ap	Sequence 15150, A	Sequence 829, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 736, App	Sequence 1634, Ap	Sequence 3, Appli	Sequence 984, App

ALIGNMENTS

TELEPHONE: (703) 413-3000 TELEFAX: (703) 413-2220 TELEX: 24885 OPAT UR INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 6911 base pairs Sequence 4, Applic Patent No. 5556776 APPLICATION NUMBER: US/08/311,174 FILING DATE: 23-SEP-1994 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION UNMBER: JP 046836/1992 FILING DATE: 04-MAR-1992 ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 556776man F. REGISTRATION UNMBER: 24,618 REFERENCE/DOCKET NUMBER: 10-699-0 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: ZIP: 22202 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: MOLECULE TYPE: TITLE OF INVENTION: SUCRASE GENE DERIVED FROM CORYNEFORM TITLE OF INVENTION: BACTERIA CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: TOPOLOGY: unknown STATE: Virginia COUNTRY: U.S.A. STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington STRANDEDNESS: ADDRESSEE: P.C. ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT INFORMATION: nucleic acid Application US/08311174 MIWA, KIYOSHI TSUCHIYA, MAKOTO (703) 413-3000 DNA (genomic) unknown Version

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61.8%; Score 3687; 100.0%; Pred. No. 0; 0; Mismatches

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961 ATACCACTACCAGCGCAATTGCCTTGGCTAAAGAGAAAAATGTGACGGTCACGGCTACGC 1020 1021 ATTTGTTCAATGCGATGCCTCCGGTGCATCATAGGGCTCCCGGCAGCGTGGGCGCTTTGC 1080	01 TCGATCTCTGCGCAGCGCACCACATCATTGCTTCCTTCGGGCACACTGATGCAGATTTTG 9	GAAAAGGTTGGATCAAATCGATCACAGTAGCGCCGGAAACTGACAATCTTTCTGAGCTTC 9	AAAACCCGGATTTCATTTTTCCCGGCAACCCAACAGATCTTGCCCGGGTGATCCATGCGG 84	GOUGH COGN TORNUM TO THE TOTAL	61 CGGCGCCGGCTGACGGCACTGGCACGGCAGGGGAAAACCTTATTCCCTTGTGGAAGAGG 72	01 GGBACACCGCGAGTATCACCGCGAACATGGCACGACCGTGATGTTGACGAAGCATGGTTT 6	41 ATCTTCATAATCACGGTGGAAACGGTGGCGCGTTTCCTACGGGAACGCAGGACCAGGCGA 6 41 ATCTTCATAATCACGGTGGAAACGGTGGCGCGTTTCCTACGGGAACGCAAGGACCAAGGCGA 6 41 ATCTTCATAATCACGGTGGAAACGGTGGCGCGTTTCCTACGGGAACGCAAGGACGAACGGAACGAAC	81 CAGCACCTAAAAACCAAGATTCCACCCCAACTCCCACCATTCTTCCCCCATTTTTATTG 5	21 GGTGATTGATGGCTTTCTCCAACTCGAAAACGGCATCATCACGGAACTCTCTGGAGAAC 4	ANGARAR TIGCRIGETCARGCAGTTARARARATITGAGGARAGARTTGTTCCCCCCCCCG 4		CAACAGCAGGCCTCAAGTCCGAAGATAATTAACCTAGATCCGTAGACATAAGACATCATA 3	TCTGCAGTTTTTAAGTTATGCATCATCAGCTTGGAAGGCTGAGGTAATTCAGTAGACCTG 24	C.C.C.C.G.L.C.G.C.G.C.G.G.G.G.G.G.G.G.G.	ACGCTCCCGTCGGCGTGGAGTGGGGTCATTACGGGTGGGATCACGCCGGTGAAAGTTGCG ACGCTCCCGTCGGCGACTGACTGCGTTACGGGTGGGATCACGCCGGTGAAAGTTGCG ACGCTCCCGTCGGCACTGCACT	1 AGTICCGTCGACGCCACCATTGATGTGGTGGTCACCGAGCTTTGCGGAGGCTTTCTACATCT 60
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RESULT 2
US-09-710-279-3464/c
US-09-710-279-3464/c
Sequence 3464, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
APPLICATION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 66/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3464
LENGTH: 2913
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: nucleic acid sequence
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Pred. No. 5.8e-62;
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEC
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 199-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5847
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US-09-489-039A-5847
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; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5847
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                                                       GGCACACGGTCTGCAGGGACTCTATGATTTCGGTGGTCCAGTCGGCGGTCTGCTTTTCGG 4713
                                                                                                                                    TGTGTTGGTTGCGCAGGATCTGTTCGGTCCGCAATCACTGGTGGAGATGTTCCCTCAGAT 4233
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Pred. No. 1.2e-46;
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US-09-489-039A-6203/c
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; Patent No. 6610836
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SEQ ID NO 6203
LENGTH: 1386
TYPE: DNA
CORGANISM: Klebsiella p
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APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT EPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF STO. 1999-01-29
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                 TCAATAAAG----TCTATGCCGCCTTTATCCAGGCCGCAGGCATCAGCGAATCGAGCAAAT
                                                 TGGATCATGTTTTCAAAGAACTCGATGACGCAACCTCCAAAGACATCGCTGTGTCCACAG
                                                                                   GGGTGAAAGGCTGCTTTCGCAATGCCGGACAGATGCAGATCATCTTCGGCACCGGGGTGG
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                                 CGGCGATCCCGGGAATGGCTATCGTGCAGGCCAGCTCGCTGCTGAACTACATTATCGGAA 108
                                                               CAGGTTTCTTGGGTGTTGTTTCTATTGATGCTCCAGATATGGTCATGTTCTTGGTTTGCG
                                                                                                 GTGCCGCCGGCGGCGTCGTGGTGTCGATGCACGTCTACATGACCGCGGTGGGCCTGA 168
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SEQ ID NO 2417
LENGTH: 1491
TYPE: DNA
ORGANISM: Enterococcus faecal:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13
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PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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Pred. No. 6.3e-46;
0; Mismatches 685
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                                                                                                                                                                                                                                                                             Sequence 56, Application US/08956171E Patent No. 6593114
GENERAL INFORMATION:
                                        Craig A. Rosen
Steven C. Barrash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureu.
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, IT
STREET: 9410 Key West Avenue
CTTY: Rockville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u> АТСТТВАТВСАСАТТВЕТТТСВАСАССЕТАААССТСААСВСАССЕТТААСССВСТВ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTGAAACTGGGCACGCTTATGACCTCAAATCAAATACTGGTGCT---
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COUNTRY: USA
ZIP: 20850
                                 STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTGGTGCTAAACAAAAAGTAAAAAAGGGAGAGGTTCTTGGAACATTTGACAGCACAGTA
                                                                                                                                                                                                                      Gil H. Choi
Patrick S. Dillon
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Best Local Simi
Matches 607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-8
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELECHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10939
 11356
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FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 30246 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3801 AACGCATCCTGCGCGACATTGGCGGCGAAGACATTGTCGCCGCCGCACACTGTGCAA 3860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                     TGGCTATCAACAATGTGTTGGTTGCGCAGGATCTGTTCGGTCCGCAATCACTGGTGGAGA
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                                                                                                                                                                                                                                                             AATTGTTGGGGGATATTTTTATACCAATATTACCTGCGATTGTGACAGCTGGTTTGTTAA
                                                                                                                                                                                                                                                                                  CGAAAGATGAAGCGAAACAAGCAGCTGCACAAAAAGGGAATCCAGTACAACGTTTGATCA
                                                                                                                                                                                                                                                                                                                                                                                           GAACAGTCGATGAAGTGTATAAGCAGTTTATTGATGAAACAGGTGCTCAAGAAGCT---T
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COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
TAGGCATAGTCTTAGGTTTGATTTTAATGCATCCGCAATTAGTATCTCAGTATGATTTGG 11415
                              TGGGCGCCGGCATTGGTATGGCGATGGTGTTCCCAACCCTGGTTAACGGCTACGACGTGG
                                                                TTTTCTTACCAGCATTAATTGGTTGGAGTAGTATGCGTGTATTTGGTGGTAGTCCGATTC
                                                                                              CGTTCTTGCCAGTGTTGGTTTGGTTTCACCGCAACCAAGCGTTTCGGTGGCAATGAGTTCC
                                                                                                                                                             TGTTCCCTCAGATCAGCGGTGTTGCTGAGATGATCAACCTGATGGCATCTGCGCCGTTCG 4280
                                                                                                                                                                                                                                                                                                                                                         ccacagagcagcrcaaagargrrgrggcraacaacgccaacrggrrcagccgrgcrgrga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGCGTTGGTCAAGGGGCAGTTTAAAGCAGACCATCAATATCAAATTGTCATTGGTCCAG
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                                                                                                                             TGTATCCACAAATTGCTGATATTTCAAACATCATTAATGTGATTGCGAGTACGGCATTTA
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Pred. No. 9.5e-44;
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US-08-781-986A-56
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                                                                                                                                                                                                       STREET: 9410 Key
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                               ZIP:
                                                                                                                                                                                                                                                                         ADDRESSEE:
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Sequence 56, Application US/08781986A
Patent No. 6737248
Patent No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus
NUMBER OF SEQUENCES: 5255
APPLICATION NUMBER: UPPLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12004 CGATATCAACGTCTTGTGTATTGGGGGCAATCGTTG
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9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus
5255
                                                                                                                                                                                         US/08/781,986A
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INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 30246 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Sim Matches 607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE, DOCKET NUMBER: PBS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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TGACTCTGCTGCTCACCGGCTTCCTTACGTTCATTGCTATTGGTCCAGCAATGCGCTGGG 4640
                                                           TTGAAAAAGGATTAAATAAAGTCGTTCACGATTCGATAAAATGTTGGTCGTTGGACCCG
                                                                                                                                                                          AAGCTGGTTACCAGGGCACCGTGCTTCCTGTGCTGGTGGTCTCTTGGATTCTGGCAACGA
                                                                                                                                                                                                                                          CCGCCACCATGACCGCGGGCGAAAATGCCAATGTGGTCCCTGTTTTGGTTTTGGATGTTTGCTC
                                                                                                                                                                                                                                                                                              TAGGCATAGTCTTAGGTTTGATTTTAATGCATCCGCAATTAGTATCTCAGTATGATTTGG
                                                                                                                                                                                                                                                                                                                               TGGGCGCCGGCATTGGTATGGCGATGGTGTTCCCCAACCCTGGTTAACGGCTACGACGTGG
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                                                                                               TCGAGAAGTTCCTGCACAAGCGACTCATGGGCACTGCAGACTTCCTGATCACCCCAGTGT
                                                                                                                                      AGTTGAATTACCAAGGTCAAGTGTTGCCAGTTTTAATTGCAGCTTACGTTCTAGCTAAAA
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49.1%; Pred. No. 9.5e-44;
ative 0; Mismatches 599;
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RESULT 8
US-09-583-110-297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHOO-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US/09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
SEQ ID NO 297
LENGTH: 1968
TYPER: NUMBER OF SEQ ID NOS: 5322
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.9%;
Best Local Similarity 46.5%;
Matches 876; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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3977 CCAGGCGATGTGGATGATGTTTTCAAAGAACTCGATGACGCAAACCTCCAAAGACATCGCT 4036
                                                                                                                                                                                                                                                                                                      GCCAAAGATCTGCTTCAGGCAATTGGAGGCAAAGAAATGTGACTGCCGTAACTCACTGT
                                                                                    TCAATTCCAGCTGTTAAAGGAACTTTTACAAATGCAGGTCAATTTCAGGTAATCAT----
                                                                                                                                      GATGATCCAGATCTGAAAGGCACCTTTGAAACTGGCGGCATGTTCCAGATCATCGTCGGG
                                                                                                                                                                                           GCGACACGGATGCGCTTTGTTTTAAGAGATGATAAGAAGGCTAATGTTAAAGCTATCGAG
                                                                                                                                                                                                                                              GCAACGCGTTTACGCCTCGTGCTCAAAGACACCAAGGATGTGGATCGCCAAAGTCTGGAT 3916
                                                                                                                                                                                                                                                                                                                                                      gcgcaacgcarccrececeacarregcegceaagacaacarrercececececacacrer
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Pred. No. 1.6e-43;
0; Mismatches 962;
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                                                                                                                                                                                                                                                                               GCTGTTCTTGGTATTACAGAGCCTGCGATCTTCGGTGTGAACCTTCGCCTGCGCTGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCATCTTCGCAACCGCATCCATGGCCAATATCGCGCAGGGTGCAGCATGTTTGGCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGTAAAATGGCTCTTCGGTGCAATTTTTGGTGCCCTCTACGCTCCATTTGTCATCACA 975
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                                                        AAGGCAGTTGCGTTGGGCGCTGCAGGTTTCTTGGGTGTTTCTATTGATGCTCCAGAT
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                                                                                                                   TTTGTTGCTGGGATGACTGGTTCAGCCCTTGCAGGCATGTTATCCGTTACTTTTAATGTA
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                                                                        GTTGGCCAGCAACTGATTCGTTTTGATATGGATGTCATTAAGGCTGCAGGTCTGGTGACA 1857
                                                                                              GCAGGGGAGCTGCTGTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTA
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US-08-961-527-201/c; Sequence 201, Application; Patent No. 6420135
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                                                                                   APPLICATION NUMBER: UPPLICATION DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                  ZIF: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Vei
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Gen
                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep
                                                                                                                                                                                                                                                                                         STATE: M
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                         STREET: 9410 Key
CITY: Rockville
                                                                                                                                                                                                                                                                                                             Maryland
                                                                                                                                                                                                                                                                                                                                             9410 Key West Avenue
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                                     A. Anders
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TOPOLOGY:
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TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 3895 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Matches 875;
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Best Local Similarity 46.5%;
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CCAGCAATGCGCTGGGTGGCTGACTTGCTGGCACACGGT---CTGCAGGGACTCTATGAT 4681
                                                                ATTTTTGTACCTTTCTTGTCATTGATTCCAGCCTTGATTTTGGCTCATACTGTTTTGGGA
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                                                                                          CTGATCACCCCAGTGTTGACTCTGCTGCTCACCGGCTTCCTTACGTTCATTGCTATTGGT
                                                                                                                                               TTGAGTCTGTCTTATCTTGAAATCTTCTGGCACAAGCATATCCCAGAAGTCATTTCTATG
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FILE REFERENCE: PATHO0.07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR TILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 463

LENGTH: 1894

TYPE: DNA

ORGANISM: Streptococcus pneumoniae

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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
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                 ACTGTATCTATGAACGGTGACGGTTTTGAAGCAAAAGTTGCTCAAGGTAATAAGGTGAAA
                                                        ACCGTAAACCTCAACGGCACGCACTTTAACCCGCTGAAGAAGCAGGGCGATGAAGTCAAA 5575
                                                                                                                                                                                 GTCTATGCACCAGCTGATGCTGAAGTTTCAATTGCCTTTTCCAACAGGGCACGCTTTTGGT
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81	B 5	Qy 3779 ATGGACCATAAGGACCTCGCGCGACGCTCCTGCGCGACATTGGCGGCGAAGACAACATT 3838
1956 CTCTTTCTTCCTAACGCTATCAACAGCTGCAAAGACCTTTCAAGGTGCTTCTAAGGTGTCTCCC 4915	S B 8	Query Match 2.8%; Score 167.8; DB 4; Length 1932; Best Local Similarity 46.8%; Pred. No. 1.2e-41; Matches 919; Conservative 0; Mismatches 962; Indels 84; Gaps 9;
4739 ACTGGTCTGCACCAGTCCTTCCCGCCAAITGAGCTGGAGCTGTTCAACCAGGGIGGA 4795	Db 0y	NAME/KEY: misc feature; ; LOCATION: (B) LŌCATION 11932; ; SEQUENCE DESCRIPTION: SEQ ID NO: 647: US-09-107-433-647
901 AGCATTCCATTTGGTTGGTTGGTTGGTTGGTGGGGTTCACCAATTGATCGTCGTG 960	₽ %	ORIGINAL SOURCE: ORGANISM: Streptococcus pneumoniae FEATURE:
841 ATTGGACCAGTITTCCACGTIGITGAAAACTACATCCTTATTGCTACAAAAAGCGATTCTT 900	§ B	HYPOTHETICAL: NO
4619 ATTGGTCCAGCAATGCGCTGGGTGGGTGACTTGCTGGCACACGGTCTGCAGGGACTCTAT 4678	γΩ.	TYPE: nucleic acid STRANDEDNESS: double
4559 GACTTCCTGATCACCCCAGTGTTGACTCTGCTGCTCACCGGCTTCCTTACGTTCATTGCT 4618	g Vy	INFORMATION FOR SEQ ID NO: 647: SEQUENCE CHARACTERISTICS: LENGTH: 1932 base pairs
4499 GTCTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCATGGGCACTGCA 4558	D Q	REFERENCE/DOCKET NUMBER: GTC-011 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (781)893-5007 ; TELEPHONE: 0817-5007
664 TICTINGGITTCATCCCIGTIGTIGGAAGGITCCGTTCTTCCAGCCTTCATC 720	B &	ATTORNEY/AGENT INFORMATION: NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
613 CTTCCAÀÀCGCTTGGGCAGTTGCTCAAGGTGGTGÀÀGTAACÀGCGATGAAC 663) B	0/03
4379 CTGGTTAACGGCTACGACGTGGCCACCATGACCGCGGGCGAAATGCCAATGTGGTCC 4438	VQ	0 4
553 GTATTTGGTGGAAATCCTGCCGTTGGTATCGTTCTTGGTATGATGCTTGTCTCTGGCTCA 612	dg ,	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/107,433 ETITING DATE: 10.1108
	Ş 5) COMPUTER: CUNKNOWN>) OPERATING SYSTEM: CUNKNOWN> COPTMARE: CINCONNOWN>
4259 CTGATGGCATCTGCGCGTTCGTGCCAGTGTTTGGTTGGTT	P 09	H H 3
463 CTTCCAG	Дb	STATE: Massachusetts COUNTRY: USA TID: 02354
4199 GGTCCGCAATCACTGGTGGAGATGTTCCCTCAGATCAGCGGTGTTGCTGAGATGATCAAC 4258	Ş	treet
4139 TTGGTTGGTGGCGTCTCTTCATGGCTATCAACAATGTGTTTGGTTGCGCAGGATCTGTTC 4198	QQ dq	NUMBER OF SEQUENCES: 5206 CORRESPONDENCE ADDRESS: THERAPEUTICS CORPORATION ADDRESSES: GENOME THERAPEUTICS CORPORATION
4079 AACTGGTTCAGCCGTGCTGTGAAGGTAITTGGCGGACATTTTCGTCCCGCTGATTCCAATC 4138	Qy da	APPLICANT: Lynn A Doucette-Stamm and David Bush TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
	Db	; Sequence 647, Application US/09107433 ; Patent No. 6800744 ; GENERAL INFORMATION:
4019 ACCTCCAAAGACATCGCTGTGTCCACAGAGCAGCTCAAAGATGTTGTGGCTAACACGCC 4078	γ	RESULT 11 US-09-107-433-647
3959 TTCCAGATCATCGTCGGGCCAGGCGATGTGGATCATGTTTTCAAAGAACTCGATGACGCA 4018	y Oy	Db 1840 GGTTCAGTTGCGAAGGGGGATGCTGATCGAAGTGAAATCTAA 1884
	ממ	QY 5696 GGCGAAATTGAAGCGGGAGCCAACCTGCTCAACGTCGCAAAGAAA 5740
3899 GATCGCCAAAGTCTGGATGATGATCCAGATCTGAAAGGCACCTTTGAAACTGGCGGCATG 3958	Qy	1780 ACAACAATGGTTATCGTTACAAATACAGCTGACTACGCTTCAGTAGCTCCAGTCGCAACA
109 AATAGTGTTGCCCACTGTGCGACTCGTCTACGTGTCAAAGATGAAGAGAAAATC 168	B &	DD 1720 GCTGGCGATGTTCTTGGAACATTTGACTCAAAAAATCGCTGCAGCTGAAACATTTGATGAT 1779 OV 5636 ACCACGCCGATTGTTGTACGAATTACAAGAAAAACCGGACCTGTAAACACTTACGGTTTG 5695
49 ATGAACAATCAGGAAATTGCAAAAAAAGTCATCGATGCCTTGGGCGGACGTGAAAATGTC 108	д Д	5576 GCAGGGGAGCTGCTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTA

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Sequence 1806, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
ITITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEC
ITITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR TILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                             RESULT 12
US-09-489-039A-1806
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TYPE: DNA
ORGANISM: Klebsiella
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                            TCCTCTACGCGCCGCTGGTGATTACCGGTGTCCACCAGACCACCCTCGCTATCGATATGC
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Pred. No. 5.8e-40;
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                                                       Query Match
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 9769 base no:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20030
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
COMPUTER: MSDOS version 6.2
                                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                            LENGTH: 9769 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
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Pred. No. 1e-36;
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Sequence 1277, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOST
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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Matches 306;
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US-09-134-001C-1277
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LENGTH: 732
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Best Local Similarity
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LOCATION: (20), (22)
OTHER INFORMATION:
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                                                                         rcaaggcagrigcgrigggcgcrigcaggririctreggrigririctarrcaargcriccag
                                                                                                                    CATTTATAGGTGCTGTTGCAGGATCAGGTATAGGTGCGGCTTATATTTCATTCTTCAAAG
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Pred. No. 7.9e-33;
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RESULT 15
US-09-107-532A-378
US-09-107-532A Application US/09107532A
; Sequence 378, Application US/09107532A
; Patent No. 6583275
; Patent No. 6583275
; GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAI NUMBER OF SEQUENCES: 7310
CCRRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
CCUNTRY: USA
ZIP: 02354
CCOMPUTER READABLE FORM:

THERAPEUTICS

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Best Local Similarity 52.5
Matches 380; Conservative
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TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 378:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 714 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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APPLICATION NUMBER: US/09/107,532A
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ORGANISM: Enterococcus faecium
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                               1841
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    2020 TGTGGAGGACAACGCTCGATTCTTCAACACCATCGAAGAGGTCCCAACCCACGCCGTCAC 2079
                                                                                             1960 CATTGAACCATCATCTTCTCTGTCAGGACTGACAAAGGTCCAGGCGCTGCACCCTAAAAC 2019
                                                                                                                                                                                    1901 CGCTGCAGAATCCGTTGAAGTTCAAATCCTTGGCATCGGCGGAAACGG-CACATCGCTTT 1959
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OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                  CAATGAACCTGGTGCTTCATTTGACGGAACGACTTCAGTAGTTGACTTAACAGAATCAAC
                                                                                                                                           CGATGCACATCCAATCGATATCCAAATCTTAGGAATCGGGCAAAATGGACATATCGGTTT
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                                                                                                                                                                                                                                                                                               471 AATCAATGCAAACAAACGATTCTTCGATAAAGCAGAAGATGTACCAACAAAAGCTGTTTC
711 GTAA 714
                                                                         CATCCTGTAGATGCACAACATGCCACCATCATCGTTGGATGAAGCAGCAGTATCCAAGCT 2259
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Search completed: March 9, 2005, 13:51:46 Job time : 960 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMS.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

0	Result No.
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94. 31.4 23.7 22.1.2 21.2 20.7 20.7 118.6 112.8 4.9	% Query Match
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9 US-09-738-626-1 1 US-09-738-626-2904 2 US-10-450-055-9 8 US-10-781-014-347 1 US-09-738-626-2905 8 US-10-781-014-413 1 US-09-738-626-2907 1 US-09-738-626-2907 1 US-09-738-626-2906 1 US-09-738-626-2906 1 US-09-738-626-2906	SUMMARIES
Sequence 1, Appli Sequence 2904, Ap Sequence 9, Appli Sequence 347, App Sequence 2905, Ap Sequence 413, App Sequence 415, App Sequence 2907, Ap Sequence 423, App Sequence 2906, Ap Sequence 9, Appli	Description

ALIGNMENTS

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US-09-738-626-1/c

(Sequence 1, Application US/09738626

publication No. US20020197605A1

[GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NALOGUCHI, HIROSHI
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
[CURRENT APPLICATION NUMBER: US/09/738,626
[CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-656-1
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Query Match

	D Q	Qу Db 2	Оу Дъ 2	Qy Db 2	Qу Ор 2	ОУ 2	Qу 2	р Qy	Qγ 2	фу 2	р Q У	. Qy	Qу 2	Оу рь 2	Qу Дъ 2	оу 2	о _у	Best Match
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TTGTTCAATC	ACCACTACC!	SATCTCTGCC	AAAGGTTGGJ AAAGGTTGGJ	AACCCGGATT AACCCGGATT	CIGCIGIGCO	GCGCCGGCTC	AACACCGCGG	CTTCATAAT(TTCATAAT(GCACCTAAA GCACCTAAA	GGGTGATTGATGG GGGTGATTGATGG	CAAGAAAAT(CAAGAAAAT(TCCTATGCT	ACAGCAGGC	TGCAGTTTT	ACCCATGGTON ACCATGGTON ACCCATGGTON ACCCATGGTON ACCCATGGTON ACCCATGATGTON ACCCATGATGATACATGATACATGATACATGATACATGATACATGATACATGATACATGATACATAC	GCTCCCGTCC ACTGCCGTCC	TCCGTCGAC	Best Local Similarity 97.1%; Matches 5793; Conservative
CGATGCCTC	GCGCAATTG	CAGCGCACC	NTCAAATCGA	TCATTTTC	GCATTCACC	ACGCACTGG	CAGTATCACC	CACGGTGGAA CACGGTGGAA	NACGCAGGAT	GCTTTCTCC	GCAGGTCAAG GCAGGTCAAG	rgctggaagg rgctggaagg	CTCAAGTCCG CTCAAGTCCG	PAAGTTATGO AAGTAATGO	STTCCTTGTG	GCGTGGAGT	SCCACCATTG	_
CGCTGCATC	CCTTGGCTA	TCGATCTCTGCGCAGCGCACCACATCATTGCTTC	TCACAGTAGO TCACAGTAGO	CCGGCAACCO	TCGAGGGCC	CAGCGCAGG	GCGAACATG	ACGGTGGCG	TCCACCCCG;	AACTCGAAA AACTCGAAA	CAGTTAAAA CAGTTAAAA	AACCAAATA AAGCAAATA	;aagataatt; ;aagataatt;	ATCATCAGC	GGTTGAGGG GGTTGAGGG	GGGGTCATT	ATGTGGTGG ATGAGGTGG	Pred. No. 0;); Mismatches
TAGGGCTCC	AGAGAAAAA 	TTCCTTCGG	GCCGGAAAC GCCGGAAAC	AACAGATCT	TTTCATCAA	GGAAAACCT	SCACGACCGT	ATCTTCATAATCACGGTGGAAACGGTGGCGCGTTTCCTACGGGAACG	VACTCCCCAC	ACGGCATCAT	VAATTGAGGG VAATTGAAGG	ACCTCAGAAA ACCTCAGAAA	ACCTAGATC	rtggaaggct Tggaaggct	AACGAGTGCG AACGAGTGCG	ACGGGTGGGA ACGGGTGGGA	TCACCGAGCT	0; nes 173;
CGCAGCGTG	ATACCACTACCAGCGCAATTGCCTTGGCTAAAGAGAAAAATGTGACGGTCACGGCTACG 	GCACACTGAT	TGACAATCTT GACAATCTT	AAAACCCGGATTTCATTTTTCCCGGCAACCAACAGATCTTGCCCGGGTGATC 	cgcatgccgt 	PATTCCCTTG	GATGTTGCCA ATGTTGGCA	GGAACGCAG	SATTGTTCCC	CACGGAACTC CACGGAACTC	aagaattgtt aagaattgtt	GATGGCAGAA GATGGCAGAA	CGTAGACATA CGTAGACATA	GAGGTAATTO GAGGTAATTO	GGTGAGAAGT GGTGAGAAGT	TCACGCCGGT	TGCGGAGGCT TGCGGAGGCT	Indels
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209 281348	203 281354	1979 CTGTCAGGACTGACAAAGGTCCAGGCGCTGCACCCTAAAACTGTGGAGGACAACGCTCGA 203	1920 GTTCAAATCCTTGGCGTGGAAACGG-CACATCGCTTTCATTGAACCATCATCTTCT 2813665 GTTCAAATCCTTGGCATCGGCGAAAACGGCACATCACTTCTTCTTCTAATGAGCCATCATCTTCTTCT	1860 CCTGATCCATACGAAGCAGCTGCAGAGTATGAGGCAAAGATCGCTGCAGAATCCGTTGAA 191	1800 2813785	1740 GATGAATACGTGGGACTAACCCGTGACGATGAAAACAGCTACTTTAAAACCATTCGCAAA	281	1620 AACAAGGGTGAACCTTGGGGCTTGCAACAGGATCCTCACCAGTGAGTACCTACC	1560 ATCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGTTGCAGTCCTAATCGCACCCTTCGCC	1501 TACTTTAAGTACGAGTAAAACTATCCTGAT-TTTAAAGGAGTCCCACCATGGAAATCACT	1441 CAAATTTTGTGGTCTTTGACTCAAACGGCCAGGTGCAAAAGGTCCATTTAGGTCATCAAG 	1381 CAACCGTCGCCGCTAAAATTCTCGGTCTTGGCGATCACGAAATCGCTAAATCCAACCCTG	1321 GTCAGTTCGTGCACCACGTGCGCAGGGTATGACGCTTATCGACGCGACCCTCCACACCT	2814325 ATGGCGTCGCCGTCTGCGCGATGGCGGCGCCATCGCCGGGGGTACCAGCACACTAGCGA	2814385 AAGCCGCCGGAATGCCAGACGGTGAGTACATTTTGGGCGTTTTGAACGTCACCGTCACCG	2814445 CCGATGGAACGGTCGAGCTGAGCTCCGAACAACGCCTTTTTCATCACGGACGCCATGG 2	1081 2814505 1141	2814565 ATTIGTTCAATGCGATGCCTCCGCTGCATCATAGGGATCCCGGCAGCGTGGGCGCTTTGC

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3119 GCGGATATGTCGTCGACAAGCTTGAAGGAACGACCTTCCGCGTCTTGCGAGGATTCAGCG 3178	2999 CCAACCTTTTTACGCTTCGCGATGAAGAAACTGGCGAAGATCTCGACGTGCTGATTTTCT 3058	2879 TATACCGCTCGACAGATCTTGAAAACTGGGAATTCTCCGGTGAAATCACCTTTGACCTCA	2759 TCGACGGACCCGCCAGCGGTTTCACACCCCATTACCGCGATCACATCATCAGCCCTGATG 2818	2639 TCTACACCGGCAACCTAAAAATTGACGGAAAGCGCCGCGCCACCCAAAACCTTGTCGAAG 2698	2519 CCGGACCGCAGCGATTGCAGTGGACGCACCTGCCCGACGCTCTTTACCCCGGATGCATCCT 2578	2813185 TCAATGATCCCAACGGAATGTACCTCGATGGCGATACCCTCCACGTCTACTACCACCACGCACG	TGCACACAGAACTTTCCAGTTTGCGCCCTGCGTACCATGTGACTCCTCCGCAGGGCAGGC		2159 GGAACTGTGGAAGGCCCAGTGACTGCTTCTTGCCCAGGTTCCATCCTGTAGATGCACAAC 2218
QY 4139 GETCCGCAATCACTGGTGGAAGATGTTCCTCAGATTGGTATGGGGATGGTTCCCCAACC 4378 Qy 4259 CTGATGGCATCTGCGCCGTTCGGGTTCTTGCCAGTGTTGGTTTCACCGCAACCAAG Qy 4259 CTGATGGCATCTGCGCGTTCGTGCCAGTGTTGGTTTCACCGCAACCAAG	2811506 2811506 4139 2811446	3959 TTCCAGATCATCGTCGGGCCAGGCGATGTGGATCATGTTTTCAAAGAACTCGATGACGCA	Qy 3839 GTCGCCGCACACTGTGCAACGCCTCGTGCTCAAAGACACCAAGGATGTG 3898	3719 GCTTTTCAACAAACATTCATGTCTGAATATTTTTGTTTTCTCCGGTTAAGGAGAAATTC 3	2811986 GCTTTCAAAGGTGACACTATTGAGAGATAAGTCATAAAAAAGGGTCTTTTGTGGCGAATT 3659 GTACAAATACTTCGCAAAATCCCCTTGATCGGACACAAATAAACAGGTTTTAATATTGTTTA 1	3539 ACGATAATACAGCCATTGAGATAACTGCAGGTGATGACAGGTTTCATTCGCTTTTCCGG 3598	Qy 3419 CTGTCCGAGTAGACATCCGAGGCAATATTTCCCTCGAGTGGGATGGTGTCCGTTTGTCTG 3478	Qy 3299 GATGGGTGCACTGCCTGACTGTCCCCGCAAGCTTCATTTGCGCAACCAAC	Qy 3239 GGCTCGTGGGCTGGATGGGGCTGCCCGCGCAGGATGATCACCCAACAGTTGCACAGGAAG 3298

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GTTTCACCAGTGAGCGGAAAGATCGTGGTGGCCTTCCCATCTGGTCACGCTTTCGCAGTC 5458
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                                                                                  ATGTTTGCCAGCGGAAAGCTTGGCTCAGGTGTTGCGATCGTCCCCACCAAGGGGCAGCTG
                                                                                                                                                                                                                                                                                          GTGCCTGCAGGAACGACCAAAGCCGAAGCAGAAGCACCCGCAGAATTTTCAAACGATTCC
                                                                                                                                                                                                                                                                                                                       GTGCCTGCAGGAACGACCAAAGCCGGAAGCAGAACCCGCAGAATTTTCAAACGATTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                            TATGGCCTTTACTTGGTTCGCCGCAACGGCAGCAGTTGATCCAGATGCAACCGCTGCTCCA 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCATGTTCTTGGTTTGCGCGGTAGTTACCTTTGTCATCGCATTCGGCGCAGCGATTGCT
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                                                                                                                                                                                     ACCATCATCCAGGCACCTTTGACCGGTGAAGCTATTGCACTGAGCAGCGTCAGCGATGCC
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                                                                                                                                               ATCTTTGACACCGGTACCCGTACGCTTCGAGATTTTTAAACCTGTTCAACCAGGTCATGCC
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GCAGTAGCGTTTGATATTTTGCGCCGCTG 2809618
                          GCAGTAGCGTTTGATATTTTTGCGCCGCTG 5967
                                                                                           ATCTTTGACACCGGTACCCGTACGCTTCGAGATTTTAAACCTGTTCAACCAGGTCATGCC
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US-09-738-626-2904

Sequence 2904, Application US/09738626

PUBLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGAWA, SATOSHI
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APPLICANT: HAYASHI, MIKIRO
APPLICANT: TATEISHI, NACKO
APPLICANT: TATEISHI, NACKO
APPLICANT: SENCH, AKIHIRO
APPLICANT: OCHIAI, KRIKO
APPLICANT: OCHIAI, KRIKO
APPLICANT: OZAKI, AKIO
APPLICANT: OZAKI, AKIO
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APPLICANT: DINUBNION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 2904
LENGTH: 1983
TYPE: DNA
J ORGANISM: Corynebacterium glutamicum
US-09-738-626-2904
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QY 4739 ACTGGTCTGCACCAGTCCTTCCCGCCAATTGAGCTGGAGCTGTTCAACCAGGGTGGATC	841 ATTGGCCAGCAATGCGCTGGGTGGGCAATGTGCTGGCACACGGTCTA 4679 GATTTCGGTGGGTCCAGTCGGGCGGTCTGCTTTTCGGTCTGGTCTACTCA	Qy 4559 GACTTCCTGATCACCCCAGTGTTGACTCTGCTGCTCACCGGCTTCCTTACG	Db 661 CTGTTTGGTTTAGATGTTGCCCAAGCCGGTTACCAGGGCACCGTGCTTCCTGGTGCTGGT Qy 4499 GTCTCTTGGATTCTGGCAACGATCGAGAAGTTCCTGCACAAGCGACTCATGGGCACTGC	OY 4379 CTGGTTAACGGCTACCACGTGGCCGCCACCATGACCGCGGGCGAAATGCCAATGTGGTC	Qy 4319 CGTTTCGGTGGCAATGAGTTCCTGGGCGCCGGCATTGGTATTGGCGATGGTGTTCCCAACC	CTTGCCAGTGTTGGTTGGTTT CTTGCCAGTGTTGGTTGGTTT	Qy 4199 GGTCCGCAATCACTGGTGGAGATGTTCCCTCAGATCAGCGGTGTTGCTGAGATGATCAA	TIGGTIGGTGGCGGTCTGCTCATGGCTATCAACAATGTGTTGGTTG	Qy 4079 AACTGGTTCAGCCGTGCTGTGAAGGTATTGGCGGACATTTTCGTCCCGC	დ -დ	Qy 3959 TTCCAGATCATCGTCGGGCCAGGCGATGTGGATCATGTTTTCAAAGAACTCGATGACGCA	Qy 3899 GATCGCCAAAGTCTGGATGATGATCCAGATCTGAAAGGCACCTTTGAAACTGGCGCATG	Qy 3839 GTCGCCGCCGCACACTGTGCAACGCGTTTACGCCTCGTGCTCAAAGACACCCAAGGATGTG	Oy 3779 ATGGACCATAAGGACCTCGCGCAACGCATCCTGCGCGCACATTGGCGGGGAAGACAACATT	Best Local Similarity 96.6%; Pred. No. 0; Matches 1915; Conservative 0; Mismatches 68; Indels
GGGTGGATCC 4798	T 900 Db 1921 T 900 Qy 5759 C 4738 Db 1981	CTTACGTTCATTGCT 4618 Qy 5639 ACGCCGATTGTTTCGAATCAGAAAACCGCACCTTAAGCATTACGGTTTGGGC 5698	G 720 S579 GGGAGCTGCTGTGTGAATTCGATATTGATGCCATTAAGGCTGCAGGTTATGAGGTAACC A 4558	TGCCAATGTGGTCC 4438	4378 Qy 5399 GTTTCACCACTGACGGAAAGATCGTGGTGGCCTTCCCATCTGGTCACGCTTTCGCAGTC	4318 Qy 5339 ATGTTTGCCAGCGGAAAGCTTGGCTCCAGGTGTCGCACCAACGAGGGCAGCTG	ი—ი	4 4	ნ—ნ 4 ლ	Ω—Ω	Oy 5039 GCAGTTGCGTTGGGCGCTGCAGGTTTCTTTGGGTGTTGTTTCTATTGATGCTCCAGATATG 5098	CTGGCGGCATG 3958 QY 4979 TACATTGGTATCGGTACCGCAGCTATCGGTGGCGCCTTTGATTGCACTCTTTGATATCAAG 5038	Qy 4919 GTTCTTGGTATTACARAGCCTGCGATCTTCGGTGTAACCTTCGCTGCGCTG	3838	1021 TTCATCTTCGCAACGGCATCTATGGCTAATATCGCCCAGGGTGCGGCATGTTTGGCAGTG

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; LOCATION: (101)...(1504); OTHER INFORMATION: RXS00315 US-10-450-055-9
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CURRENT APPLICATION NUMBER: US/10/450,055

CURRENT FILING DATE: 2003-06-10

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PATENTIN Vers. 2.0

SEQ ID NO 9

LENGTH: 1527
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Best Local Similarity
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TYPE: DNA
ORGANISM: Corynebacterium
FEATURE:
NAME/KEY: CDS
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   GGCAGTTGCGTTGGGCCTGCAGGTTTCTTGGGTGTTTCTATTGATGCTCCAGATAT 5097
                                                               CTACATTGGTATCGGTACCGCAGCTATCGGTGGCGCTTTGATTGCACTCTTTGATATCAA
                                                                                                                                                                                                                 GTTCTTCCTAGCGAAGAGTGAAAAGCTCAAGGGCCTTGCAGGTGCTTCAGGTGTCTCCGC
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Pred. No. 0;
0; Mismatches
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APPLICANT: Schröder, Hartwig
APPLICANT: Aberhauer, Gregor
APPLICANT: Haltwig
APPLICANT: Haltwig
APPLICANT: Haltwig
APPLICANT: Haltwig
APPLICANT: Haltwig
APPLICANT: Holerhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENC
TITLE OF INVENTION: PRODUCTION
FILE REFERENCE: BGI-126CPCN
FILE REFERENCE: BGI-126CPCN
CURRENT APPLICATION NUMBER: US/10/781,014
CURRENT FILING DATE: 2004-02-17
PRIOR APPLICATION NUMBER: US/9/602,740
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/143,208
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US-10-781-014-347
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                                                                                                                                                                                                                                                                                                      Sequence 347, Application US/10 Publication No. US20040180408A1 GENERAL INFORMATION:
                                                                                                                                                                                                                               APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkharo
APPLICANT: Schroder, Hartw
APPLICANT: Zelder, Oskar
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; LOCATION: (101)..(1342)
; OTHER INFORMATION: RXA00041
US-10-781-014-347
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Best Local Similarity
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ORGANISM: Corynebacterium
FEATURE:
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LENGTH: 1342
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OR APPLICATION NUMBER: DE 19931413.6
OR APPLICATION NUMBER: DE 19931413.6
OR APPLICATION NUMBER: DE 19931419.5
OR FILING DATE: 1999-07-08
OR APPLICATION NUMBER: DE 19931420.9
OR FILING DATE: 1999-07-08
OR APPLICATION NUMBER: DE 19931424.1
OR FILING DATE: 1999-07-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1999-07-09
APPLICATION NUMBER: 60/151,572
FILING DATE: 1999-08-31
APPLICATION NUMBER: DE 19931412.8
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                                                                                                                                                                                    Sequence 2905, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCH, HIROSHI
APPLICANT: MIZOGUCH, HIROSHI
APPLICANT: MIZOGUCH, WIKIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKHIRO
APPLICANT: TATEISHIANACHIRO
APPLICANT: TATEISHIANACHIRO
APPLICANT: SENOH, AKHIRO
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APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 2905
LENGTH: 1299
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
US-09-738-626-2905
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                                                                                                          GCTCTGACCAGTGCGGATATGTCGTCGACAAGCTTGAAGGAACGACCTTCCGCGTCTTGC
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                                                                                                                                     APPLICANY: LEGET, ORACE
TITILE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PRO:
TITILE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
TITILE OF INVENTION: PRODUCTION
FILE REFERENCE: BGI-126CPCN
CURRENT APPLICATION NUMBER: US/10/781,014
CCURRENT PILING DATE: 2004-02-17
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 60/143,208
PRIOR PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/151,572
PRIOR APPLICATION NUMBER: 60/151,572
PRIOR APPLICATION NUMBER: 60/151,572
PRIOR APPLICATION NUMBER: DE 19931412.8
PRIOR PILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931420.9
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US-10-781-014-413
; Sequence 413, Application US/10781014
; Publication No. US20040180408A1
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NUMBER OF SEQ ID NOS: 784
SEQ ID NO 413
LENGTH: 1287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwi
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Greg
    ORGANISM: Corynebacterium glutamicum
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Best Local Similarity 97.6%;
Matches 1256; Conservative
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               CGATGGAACGGTCGATCTAGCTCGTTCCAACAACGCCTTTTTCATCACGGACGCCATGGA
                                                            TGCTGCGGCACGTGCCGGGGACGCATATGTTGAGTTGATCGCCGACGGCGTGCATTTGGC
                                                                                                                TTTGTTCAATGCGATGCCTCCGCTGCATCATAGGGCTCCCGGCAGCGTGGGCGCTTTGCT
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Pred. No. 0;
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APPLICANY: SCHTOUGE, DALLALY
APPLICANY: Haberhauer, Gregor
TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROT
TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROT
TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
TITLE OF INVENTION INVEST: US/10/781,014
CURRENT FILING DATE: 1004-02-17
PRIOR APPLICATION NUMBER: US/10/31
PRIOR APPLICATION NUMBER: 06/141,031
PRIOR APPLICATION NUMBER: 06/141,031
PRIOR APPLICATION NUMBER: 06/143,208
PRIOR APPLICATION NUMBER: 05/1931412.8
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
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APPLICANT: Pompejus,
APPLICANT: Kroger, F
APPLICANT: Schroder
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Query Match 20.7%; Score 1237.4; Best Local Similarity 97.6%; Pred. No. 0; Matches 1256; Conservative 0; Mismatches
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                                                                          TTTGTTCAATGCGATGCCTCCGCTGCATCATAGGGCTCCCGGCAGCGTGGGCGCTTTGCT
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RESULT 9
US-10-781-014-423
; Sequence 423, Application US/10781014
; Publication No. US20040180408A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
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APPLICANY: Belder, Oskar

APPLICANY: Alberhauer, Gregor

TITLE OF INVENTION: CONNUEBACTERIUM GLUTAMICUM GENES ENCODING PROT

TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY

TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY

TITLE OF INVENTION: PRODUCTION

FILE REFERENCE: BGI-126CPCN

CURRENT FILING DATE: 2004-02-17

PRIOR APPLICATION NUMBER: US/10/781,014

CURRENT FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: 60/141,031

PRIOR APPLICATION NUMBER: 60/143,208

PRIOR FILING DATE: 1999-07-09

PRIOR FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: 60/143,208

PRIOR APPLICATION NUMBER: 60/143,208

PRIOR APPLICATION NUMBER: 60/143,208

PRIOR APPLICATION NUMBER: DE 19931412.8

PRIOR APPLICATION NUMBER: DE 19931413.6

PRIOR APPLICATION NUMBER: DE 19931413.6

PRIOR APPLICATION NUMBER: DE 19931419.5

PRIOR APPLICATION NUMBER: DE 19931420.9

PRIOR APPLICATION NUMBER: DE 19931424.1

PRIOR APPLICATION NUMBER: DE 19931424.1

PRIOR APPLICATION NUMBER: DE 19931428.4

PRIOR APPLICATION NUMBER
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Best Local (
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Local Similarity 93.0%;
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                              TGACCACATCGACATCGATTGATGAAGAGGTCTACAGCCCCAGATGGTGCAAACCCCTGATCC
                                                                                                                                                                                                                                                                                                                     CGGAACCTTGGGGCTTGCAACTGGATCGTCACCTTTGAGCACCTACCAAGAGCTCATTCG
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TGACCACATCGACATCGTTGATGAAGAGGTCTACAGCCCAGATGGTGCAAACCCCTGATCC
                                                                                                          CGTGGGATTAACGCGCGACGATGAAAACAGCTACTTCAAAACCATTCGTAAAGAGTTCAC
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Zelder, Oskar
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Pred. No. 2e-223;
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APPLICANT: ANUO, SELECTION APPLICANT: HAYASHI, MIKIRO
APPLICANT: COCHIAI, KEIKO
APPLICANT: YOKOI, HARHHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIHIRO
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 09/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 2906
LENGTHARE: PATENTIN VET: 3.0
SEQ ID NO 2906
LENGTH: 759
TYPE: DNA
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US-09-738-626-2906
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                                                                        Query Match
Best Local Similarity
Matches 711; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSI
                                                                                                                                                                     TYPE: DNA
ORGANISM: Corynebacterium
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                      1548 ATGGAAATCACTATCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGTTGCAGTCCTAATC 1607
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  ATGGACATCATCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGCGGCAGCCCTGATC
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                                                                            Conservative
                                                                                            11.3%;
93.7%;
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                                                                          Score 671.8; DB 9;
Pred. No. 1.3e-195;
0; Mismatches 47;
                                                                            Indels
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Sequence 9. Application US/10494541

; Publication No. US20050009152A1
; Publication No. US20050009152A1
; GENERAL INFORMATION:
APPLICANT: Ealder, Oskar
; APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Klopprogge, Corinna
APPLICANT: Klopprogge, Corinna
APPLICANT: Klopprogge, Corinna
APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: Genes coding for proteins for genetic stability,
TITLE OF INVENTION: Gene scoding for proteins for genetic stability,
TITLE OF INVENTION: Gene expression and folding
; FILE REFERENCE: BGI-166US
; CURRENT APPLICATION NUMBER: US/10/494,541
; CURRENT APPLICATION NUMBER: US/10/494,541
; CURRENT FILING DATE: 2002-10-33
; PRIOR APPLICATION NUMBER: PCT/EP02/12138
; PRIOR APPLICATION NUMBER: DE 10154180
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 104
; SEQ ID NO 9
; LENGTH: 1543
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US-10-494-541-9
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LENGTH: 1543

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APPLICANT: Kim, Jun-Won
APPLICANT: Lee, Heung-Schick
APPLICANT: Lee, Heung-Schick
APPLICANT: Hwang, Byung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/60740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 09/60114
PRIOR APPLICATION NUMBER: 09/60114
PRIOR APPLICATION NUMBER: 09/60114
PRIOR APPLICATION NUMBER: 60/141031
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
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; OTHER INFORMATION: RXA00314
US-10-494-541-9
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                                                                                     NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn Vers. 2.0
SEQ ID NO 31
LENGTH: 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 31, Application US/09746660A Publication No. US20030049804A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 294;
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Best Local Similarity
                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/142101
PRIOR TILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19931420.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwi
                                                                                                                                                                            PRIOR FILING DATE: 1999-07-08
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
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ORGANISM: Corynebacterium glutamicum
                                                                    TYPE: DNA
                                         ORGANISM: Corynebacterium glutamicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5854 TAAACCTGTTCAACCAGGTCATGCCTCGGTGTACCTGTGTGGTGCCACCCCGCAATCTTC
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Zelder, Oskar
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; Pred. No. 8.4e-79;
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                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,12
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                     PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2011-02-09
PRIOR FILING DATE: 2011-02-09
                                         Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17961
LENGTH: 777
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Matches
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Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
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APPLICANT:
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                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
TYPE: DNA ORGANISM: Cornyebacterium diptheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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Carr, Grant
Carr, Grant
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Zyskind, Judith
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Malone, Cheryl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.6%;
ilarity 96.5%;
Conservative
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lio, Carlos
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Pred. No. 1.4e-54;
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                                                                                                                               See File Wrapper or
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RESULT 14
US-10-282-122A-17959
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                                                                                                                                                                                                                                   Sequence 17959, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                               APPLICANT:
                                                                                                          APPLICANT:
                                                                                                                                                         APPLICANT: Wang,
APPLICANT: Zamud
APPLICANT: Malor
                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1608 GCACCCTTCGCCAACAAGGGTGGAACCTTGGGGCTTGCAACAGGATCCTCACCACCTGAGT 1667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1548 ATGGAAATCACTATCTGCAAAGACGAGCAAGAAGTCGGCAAAGCAGTTGCAGTCCTAATC 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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                                               Zamúdio, Čarlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCACACTCAGTACTACCG
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                               Trawick, John
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       Grant
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57.8%;
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Pred. No. 1.9e-52;
0; Mismatches 305;
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APPLICANT: Ku, H.
APPLICANT: Ku, H.
TITLE OF INVENTION: Identification of Essential Genes in PILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/2191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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Best Local Similarity 53.5%;
Matches 433; Conservative
                                                                                                  931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254
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AAGAGAAAAATGTGACGGTCACGGCTACGCATTTGTTCAATGCGATGCCTCCGCTGCATC 1050
                                               TCTCCCTCGGACACCGACGCAGACTTCTCAGTCACCGAACAAGCCCTGTCCTACGCAG 673
                                                                                                  CTTCCTTCGGGCACACTGATGCAGATTTTGATACCACTACCAGCGCAATTGCCTTGGCTA
                                                                                                                                                                                         CGCCGGAAACTGACAATCTTTCTGAGCTTCTCGATCTCTGCGCAGCGCACCACCATCATTG
                                                                                                                                                                                                                                                                                              CAACAGATCTTGCCCGGGTGATCCATGCGGGAAAAGGTTGGATCAAATCGATCACAGTAG
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                                                                                                                                                    CCCCCGAAACCGCCACGCCAAGGAAATCATCGACCTCTGCGCCGAAAAACAACATCATCG
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Pred. No. 1.4e-47;
0; Mismatches 364; Indels 12;
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433

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APPLICANT: Berka, Randy M.

APPLICANT: Clausen, Ib Groth
ITITE OF INVENTION: Methods For Monitoring Multiple Gene
ITITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FRESEQ for Windows Version 4.0
SEQ ID NO 829
LENGTH: 975
TYPE: DNA
ORGANISM: Bacillus licheniformis
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US-09-974-300-829
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Best Local Similarity 51.4%;
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                                        GGTGCTTCCCATTTTGCTCGCTTCTTATTTGCTGGCAAAAATTGAGCGCTTTTTGACAAA
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                              CATCGCATTCGGCGCAGC 5151
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Search completed: March 9, 2005, 20:15:11
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1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7
984	934	905	812	746	875	917	892	949	1003	847	669	1040	2229	1114	1063	1051	1049	1033	872	870
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BU167870	BQ929688	BU179037	BI825295	BI758774	BU158666	BX428009	CR713846	BX324827	AL546345	BU171522	BE790435	AL152142	CR609510	BX421863	BM910583	BM476096	BX406188	AL560879	BX374555	AY416649
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REFERENCE AUTHORS VERSION KEYWORDS BZ685850/c Ś 밁 ORIGIN FEATURES COMMENT SOURCE ACCESSION DEFINITION ORGANISM Matches 483; Query Match TITLE source Loca1 3930 TGAAAGGCACCTTTGAAACTGGCGGCATGTTCCAGATCATCGTCGGGCCAGGCGATGTGG 914 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (Dases 1 to 917) Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Wanielaw, C.A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Maize Genomics Consortium Unpublished (2003) Contact: Cathy Whitelaw BZ685850 PUBEE66TD ZM_0.6_1.0_KB genomic survey sequence BZ685850 9712 Medical Center Drive, Tel: 301-838-5843 Zea mays BZ685850.1 Class: sheared ends. Seq primer: TF Email: whitelaw@tigr.org Fax: 301-838-0208 Bennetzen, J. Zea mays Similarity 52. 83; Conservative TCAAGGGTTCGTTCTTCACCGGCGGGGCTGTTCCAGGTGGTAATCGGCCCCCGGTGAAGTGG /clone="ZMMBTa035K11" /clone_lib="ZM_0.6_1.0_KB" /note="Vector: pCR4-TOPO; Site_1: CoT selected genomic DNA library" Location/Qualifiers /strain="B73" /db_xref="taxon:4577" organism="Zea mays" mol_type="genomic DNA" 2.9%; 0 Score 174.8; DB 8 Pred. No. 3.4e-39; 0; Mismatches 412 Zea Rockville, MD 20850, USA mays đđ DNA linear GSS 05-FEB-2003 genomic clone ZMMBTa035K11, 412; 8 Length EcoRI; 0.6-1.0 kb high Indels 917; 21; Gaps 855 3989 4.

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RESULT 2
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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Veterinary Biomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH
Email: j.hopkins@ed.ac.uk
Plate: 04 row: M column: 09
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Gossner,A. and Hopkins,J.
Ovine spleen|brain cDNA library
Unpublished (2004)
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                                                                                          CCCGGTGACCCGTCACCTCGGCATCCTGATCACCGAAGGCGTGGTCACTCTGTTTGACCT
                                                                                                                                                          TCCAGCAATGCGCTGGGTGACTTGCTGGCACACGGTCTGCAGGGACTCTATGATTT
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/clone_lib="Sheep spleen\brain
/note="Vector: pSport1"
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/mol_type="mRNA"
/db_xref="taxon:9940"
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Matches 346; Conserv
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  1666 GTACCTACCAAGAGCTCATTCGCATGTATGAAGCTGGGGAAGTGTCATTCAAGAACTGCA 1725
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CDA98-D12.yld-s SHGC-CDA Gasterosteus aculeatus CDNA clone
CDA38-D12 3', mRNA sequence.

CDA99281

CD499281. GI:31426312

EST.

Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Gasterosteus aculeatus
ENkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HHMI and Department of Developmental Biology Stanford University School of Medicine Beckman Center B300, 279 Campus Drive, Stanforel: 650 725 5954 Fax: 650 725 7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arightey, D.m., Felchel, C., Balabandra, S., Grimwood, Schmutz, J. and Myers, R.M.
Expressed sequence tags from Gasterosteus aculeatus Unpublished (2003)
Contact: Kingsley, DM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kingsley, D.M.
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                                                                                 TCGCACCCTTCGCCAACAAGGGTGGAACCTTGGGGCTTGCAACAGGATCCTCACCACTGA 1665
                                         TCCGACCTGGTCCGGACAGATTTTTTACCCTGGGGCTTCCCACAGGAAGCACCCCAATGG 712
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                                                                                                                               Conservative
                                                                                                                                                                                                                           /Clone lib="SHGC-CDA"
//Clone lib="SHGC-CDA"
//Clone lib="SHGC-CDA"
//Clone lib="SHGC-CDA"
//Clone lib="SHGC-CDA"
//Clone lib="Site_2: XhoI (3' linker primer); The mixed
(5' adaptor); Site_2: XhoI (3' linker primer); The mixed
organ cDNA library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a a 50 bp linker primer containing an oligo dT sequence
preceded by a synthetic XhoI site. 5 prime adaptors were
used containing an EcoR1 cohesive end. The finished cDNAs
were inserted in to the ZAP express vector
unidirectionally in the sense orientation with respect to
the lac2 promoter of pBK-CMV. An amplified library was
prepared from approximately 3 million primary clones in
the lambda ZAP Express vector. In vivo excision was then
used to generate individual pBK-CMV phagemid clones for
EST sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="heads and internal organs combined"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="CDA38-D12"
/sex="mixed male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Salinas river,
/db_xref="taxon:69293"
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                                                                                                                          2.1%; Score 123.6; DB 6; 52.3%; Pred. No. 4.7e-24; tive 0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type="mRNA"
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Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Gasterosteus aculeatus
Gasterosteus aculeatus
Gasterosteus aculeatus
Gasterosteus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
                                                                                                                                                                                                                                                        Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD499280 1030 bp mRNA linear EST 12 CDA38-D12.xld-t SHGC-CDA Gasterosteus aculeatus cDNA clone CDA38-D12 5', mRNA sequence.
                                                                                                                                                   HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD499280
CD499280.1 GI:31426311
                                                                                                       Tel: 650 725 5954 Fax: 650 725 7739
                                                                       Email: kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                     Contact: Kingsley, DM
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quality sequence stop: 822
Location/Qualifiers
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                                                                                                                                                           CA 94305-5329, USA
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CCGCTTTCCAGCAGCACCCGCAGACAGTTTTTGTGTGTGATGAAGACGCCACATTGGAAC
                                           CCATCCTGTAGATGCACAACATGCCACCATCATCGTTGGATGAAGCAGCAGTATCCAAGC
                                                                                               ACAAGGCCTTTGCCTTATACAAAGCTATAGAGGAAGGTGTGAATCACATGTGGACAGTGT
                                                                                                                                             GAAAAGCCGACGCCATCCGCGGAACTGTGGAAGGCCCAGTGACTGCTTCTTGCCCAGGTT
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                                                                                                                                                                                                CGGTGGGAGTGGCACAGTCATGGACGCAAAAGAGGTCCTGATTCTCATCACTGGAGCAC
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/dev stage="adult"
/clone_lib="SHGC-CDA"
/clone_lib="SHGC-CDA"
/note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRl
/note="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRl
(5' adaptor); Site 2: XhoI (3' linker primer); The mixed
organ cDNA library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a a 50 bp linker primer containing an Oligo dT sequence
preceeded by a synthetic XhoI site. 5 prime adaptors were
used containing an EcoRl cohesive end. The finished cDNAs
were inserted in to the ZAP express vector
unidirectionally in the sense orientation with respect to
the lac2 promoter of pBK-CMV. An amplified library was
prepared from approximately 3 million primary clones in
the lambda ZAP Express vector. In vivo excision was then
used to generate individual pBK-CMV phagemid clones for
EST sequencing."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:69293"
/clone="CDA38-D12"
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|mol_type="mRNA"
|strain="Salinas river, CA"
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Graduate School of Science, University of Tokyo;
Science and Technology Corporation, Japan
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-03-5841-4434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 745)
Osada,S., Kitayama,A., Ueno,N. and Taira,M.
Expression analysis of genes which are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP705177 Osada Taira anterior neuroectoderm (ANE) pCS105 cDNA library Xenopus laevis cDNA clone XL514b2lex 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroectoderm of Xenopus embryos
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP705177
BP705177.1 GI:46053576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Masanori Taira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
                       TTCGGGCTGCTGGTGGCATTGAACTGTTTGTTGGAGGTATCGGTCCTGATGGTCACATAG
                                                                  T---CGCTGCAGAATCCGTTGAAGTTCAAATCCTTGGCATCGG-CGGAAACGGCACATCG 1955
                                                                                                                                                                    ACAGCCCAGATGGTGCAAACCCTGATCCATACGAAGCAGCTGCAGAGTATGAGGCAAAGA 1899
                                                                                                                                                                                                                     ATCATTCCTTCATGTGGAACAACTTCTTTAAGCACATTGACATCAGAGGTGAGAATGCCC 359
                                                                                                                                                                                                                                                                   ACTTTAAAACCATTCGCAAAGAGTTCACTGACCACATCGACATCGTTGATGAAGAGGTCT 1839
                                                                                                                                                                                                                                                                                                                      ATGTGAAAACATTCAATATGGATGAGTATGTTGGCCTTCCCAGGGAGCACCCAGAGAGCT
                                                                                                                                                                                                                                                                                                                                                                     ACTGCAAGGCATTCTTGTTGGATGAATACGTGGGACTAACCCGTGACGATGAAAACAGCT 1779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTGAGTACCTACCAAGAGCTCATTCGCATGTATGAAGCTGGGGGAAGTGTCATTCAAGA 1719
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llarity 52.2%;
Conservative
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/dev_stage="late gastrula (stage 12.5)"
/clone_lib="Ogada Taira anterior neuroectoderm
pCS105_cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL514b2lex"
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Pred. No. 4.5e-21;
0; Mismatches 291;
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                                                ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15095 row: a column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog) Xenopus laevis
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EST.
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AGENCOURT 19145816 NICHD XGC Te2 Xenopus laevis cDNA
IMAGE:7208717 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Igor B. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Amphibia; Batrachia; Anura; Mesobatrachia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGTTCCATCCTGTAGATGCAC 2215
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Location/Qualifiers
                                                   /dD_xtel="cacul-
/clone="IMAGE;7208717"
/clone="IMAGE;7208717"
/lab host="DH10B TonA"
/lab host="DH10B TonA"
/clone lib="NICHD KGC Te2"
/note="Organ: testis; Vector: pExpress-1; Site_1: EcoRV;
Site_2: NotI; RNA obtained from 6 adult male testis. cDNA
was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGGCCCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1kb
resulted in an average insert size of 1.25 kb. This is a
primary library (normalized primary library is
NICHD_XGC Te2N) and was constructed by Express Genomics
(Frederick, MD). Note: this is an NIH_XGC library"
                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:8355"
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ence stop: 707.
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KEYWORDS
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TITLE
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Emaīl: cgapbs-r@mail.nih.gov
Tissue Procurement: Igor B. Dawid
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKBUS/15
760 bp mRNA linear EST 26
AGENCOURT 19145650 NICHD_XGC_Te2 Xenopus laevis cDNA clone
IMAGE:7210866 5', mRNA sequence.
                                                                                                                                                                            National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20
                                                                                                                                                                                                                       Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
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                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
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0; Mismatches 245
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Best Local Similarity
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5'-pgAcTAGTTCTAGATCGCGAGCGCCCC(T)25-3' and cloned int
the EcoRV/NoI sites of pExpress-1. Size-selection >1kb
resulted in an average insert size of 1.25 kb. This is
primary library (normalized primary library is
NICHD_XGC_Te2N) and was constructed by Express Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="NICHD_XGC_Te2"
/note="Organ: testis; Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI; RNA obtained from 6 adult male testis. cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Pooled samples
/lab_host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Xenopus laevis"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:8355"
/clone="IMAGE:7210866"
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Pred. No. 1.4e-20;
0; Mismatches 282;
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AUTHORS
TITLE
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Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 899)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zo
Sanger Xenopus tropicalis EST project 2001
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX714658
BX714658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                constructed by Nigel Garrett.

cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 will EcoRI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

Host: Escherichia coli DH10B.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TTpA015j16.plkSP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing primer: $P6
This sequence is from a Xenopus Gene Collection (XGC) library
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  CCATCATCTTCTCTGTCAGGACTGACAAAGGTCCAGGCGCTGCACCCTAAAACTGTGGAG
                                                                                          TCCGTTGAAGTTCAAATCCTTGGCA----TCGGCGGAAAACGGCACATCGCTTTCATTGAA 1966
                                                                                                                                                                                      GGTGCAAACCCTGATCCATACGAAGCAGCTGCAGAGTATGAGGCAAAGATCGCTGCAGAA 1910
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                                                  GGTGGGATTGAGCTGTTTGTTGGAGGTATTGGTCCTGATGGCCACATAGCTTTTAATGAG
                                                                                                                                              GGAAATGCCACAGACCTTCAGGCAGAGTGTGACCTGTTTGAAGAAAAAGATTCGGGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="XGC-tadpole"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from tadpole
embryos. EcoRI-NotI cut cDNA was then ligated into pCS10
with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridgeshire,
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/mol_type="mRNA"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="TTPA015j16"
/dev_stage="tadpole (stage
/lab_host="E. coli_DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Rob Granger, University of Virginia
cDNA Library Preparation: Open Blogystems
cDNA Library Preparation: Open Blogystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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AGENCOURT_15227262 NICHD_XGC_SwblN Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence start: 15 quality sequence stop: 717. Location/Qualifiers
                           /note="Vector: pExpress:1; Site 1: ECORV; Site 2: NotI; Bulk tissue was collected from a whole 10 month old male from the F6 strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1.5 kb fragments for an average insert size of 1.92 kb. Library was normalized to Cot5 with a 180-fold reduction of actin. A non-normalized version of this library is also available (NICHD_XGC_Swb1). Library was constructed by Open Biosystems (Huntsville, AL). PLEASE NOTE: This library contains high level of
                      contamination
                                                                                                                                                                                                                                                                                                          /tissue_type="whole_body"
/clone_lib="NICHD_XGC_Swb1N"
                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:6998096"
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                                                                                                                                                Xenopus tropicalis

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to, 896)
              Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH Bldg. 31 RM10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                AGENCOURT 15680772 NICHD XGC Swbin IMAGE:7024229 5', mRNA sequence. CF592490
                                                                                                     Unpublished (1999)
                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
Tissue Procurement: Rob Granger, University of Virginia
                                                                                                                                                                                                                                                                                       CF592490.1 GI:36345132
                                                                                                                                                                                                                                                Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTAGATGCAC 2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCGACGCCATCCGCGGAACTGTGGAAGGCCCAGTGACTGCTTCTTGCCCAGGTTCCATC
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Pred. No. 2.2e-18;
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FEATURES
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Best Local Similarity
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14753 row: f column: 03
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                                                   gccgacgccarccgcggaacrgregaaggcccagrgacrgcrrcrrgcccaggrrccarc
                                                                                                                                                                                                                                                                                    GACAACGCTCGATTCTT---CAACACCATCGAAGAGGTCCCAACCCACGCCGTCACCCAG
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GCATTTGCTTTGTATAAGGCAATTGAGGAAGGTGTAAATCATATGTGGACAGTTTCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contamination by worm"
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/clone_lib="NICHD_XGC_Swb1N"
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/mol_type="mRNA"
/db_xref="taxon:8364"
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50.5%;
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Pred. No. 2.3e-18;
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Matches 324; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage ; 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) The sequences are based on single pass reads.

More information available at http://www.genoscope.cns.fr/tetraodon.
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Tetraodon nigroviriāis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1177 bp
Tetraodon nigroviridis full-length
CR696680
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HTC; cDNA; full-length; Tetraodon nigroviridis
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TCACCCAGGGTTTGGGCACTTTGTCCCGCGCGCAAAACATCGTGTTGGTGGCAACTGGTG
                                                                                                                                                                             TGGAGGCTGGTGGGATCCAGCTGTTTGTCGGAGGAATTGGACCGGACGGCCACATTGCCT
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                                                                                                         TCAACGAGCCCGGTTCCAGTTTGGTGTCCAGAACGCGGGTGAAGACCCCTGGCCAAGGACA
                                                                                                                                                                                                              CTGCAGAATCCGTTGAAGTTCAAATCCTTGGCA----TCGGCGGAAACGGCACATCGCTT
                                                                                                                                                                                                                                                  TTTTAGATGGCAACGCCGACCTGCAGGAGGAGTGCGAAGCCTTCGAGAGGAAGATTG
                                                                                                                                                                                                                                                                                   GCCCAGATGGTGCAAACCCTGATCCATACGAAGCAGCTGCAGAGTATGAGGCCAAAGATCG
                                                                                                                                                                                                                                                                                                                      ACTCCTTCATGTGGAGCAACTTCTTCAAGCACATCGACATCAAGGCGGAAAACACTCACA
                                                                                                                                                                                                                                                                                                                                                       TTAAAACCATTCGCAAAGAGTTCACTGACCACATCGACATCGTTGATGAAGAGGTCTACA
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                                   CCATCATTGCCAACGCGCGTTCTTTGACGGGGACCTCTCCAAAGTGCCCACCAACGCCC
                                                                    CTGTGGAGGACAACGCTCGATTCTTCAAC---ACCATCGAAGAGGTCCCAACCCCACGCCG 2075
                                                                                                                                          TCATTGAACCATCATCTTCTCTGTCAGGACTGACAAAGGTCCAGGCGCTGCACCCTAAAA
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/mol type="mRNA"
/db_xref="taxon:99883"
/tissue_type="Eyes"
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Pred. No. 2.5e-:
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Best Local Sim:
Matches 324;
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The sequences are based on single pass reads.
More information available at http://www.genoscope.cns.fr/tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTC; cDNA; full-length; Tetraodon nigroviridis. Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                          GCCCAGATGGTGCAAACCCCTGATCCATACGAAGCAGCTGCAGAGTATGAGGCAAAGATCG
                                                                                                                                                                                                                                                                                                                                                                        GCAAGGCATTCTTGTTGGATGAATACGTGGGACTAACCCGTGACGATGAAAACAGCTACT
                                        TCATTGAACCATCATCTTCTCTGTCAGGACTGACAAAGGTCCAGGCGCTGCACCCTAAAA 2018
                                                                                                                             CTGCAGAATCCGTTGAAGTTCAAATCCTTGGCA----TCGGCGGAAACGGCACATCGCTT
                                                                                                                                                                                                                                                   ACTCCTTCATGTGGAGCAACTTCTTCAAGCACATCGACATCAAGGCGGAAAACACTCACA
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/mol_type="mRNA"
/db_xref="taxon:99883"
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Pred. No. 2.5e-18;
0; Mismatches 321;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at http://www.genoscope.cns.fr/tetraodon.
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HTC; cDNA; full-length; Tetraodon nigroviridis
Tetraodon nigroviridis
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CR701935.1
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Tetraodon nigroviridis full-length
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  CTGCAGAATCCGTTGAAGTTCAAATCCTTGGCA----TCGGCGGAAACGGCACATCGCTT 1958
                                           TTTTAGATGGCAACGCCGCCGACCTGCAGGAGGGAGTGCGAAGCCTTCGAGAGGAAGATTG
                                                                                                                                                                                                                                                 GCAAGGCATTCTTGTTGGATGAATACGTGGGACTAACCCGTGACGATGAAAACAGCTACT
                                                                                                                                                                                                                                                                                                                                 TGAGTACCTACCAAGAGCTCATTCGCATGTATGAAGCTGGGGAAGTGTCATTCAAGAACT
                                                                                                                                                                 TTAAAACCATTCGCAAAGAGTTCACTGACCACATCGACATCGTTGATGAAGAGGTCTACA 1842
                                                                                    GCCCAGATGGTGCAAACCCTGATCCATACGAAGCAGCTGCAGAGTATGAGGCAAAGATCG
                                                                                                                          ACTCCTTCATGTGGAGCAACTTCTTCAAGCACATCGACATCAAGGCGGAAAACACTCACA 587
                                                                                                                                                                                                            TGAAGACCTTCAACATGGACGAATACGTTGGTCTCCCCAGGGACCACCCCGAGAGCTACC
                                                                                                                                                                                                                                                                                          TGGGTTGCTACAAGAAGCTGATCGAGTATTACAAGAATGGAGAAGTCTCGTTTCGGTACG
                                                                                                                                                                                                                                                                                                                                                                          TATTCAATCCCGGCCCGGACCGGTATTTTACCCTGGGGCTGCCCACAGGAAGCACTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Tetraodon nigroviridis"
/mol type="mRNA"
/db xref="teaxon:99883"
/tissue_type="Byes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 104.4; DB 3; Pred. No. 2.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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CDNA
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BM017859
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ORGANISM
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VERSION
                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
     Query Match
Best Local Similarity
Matches 327; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 to 818)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM017859
603645335F1 NIH_MGC_98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://image.iii.yv.
Plate: LLCM1892 row: e column:
Plate: -1:tv semience stop: 803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM017859
BM017859.1 GI:16532213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTCTGCCTTCCAGCAGCACCCACAGTCCATCTTCGTGTGCGACGAGGACGC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGGAAAAGCCGACGCCATCCGCGGAACTGTGGAAGGCCCAGTGACTGCTTCTTGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTCCATCCTGTAGATGCACAACATGCCACCATCATCGTTGGATGAAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACACAAGGCTCTGGCCTTTGGCCAAAGCTATCGAGGAGGGCGTGAATCACATGTGGACCG
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     1.7%;
ilarity 49.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: Location/Qualifiers
                                                                                                                 /tissue_type="matrocytoma grade IV, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 98"
/clone lib="NIH MGC 98"
/clone Torgan: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
/mote="Organ: brain; Vector: poTB7; Site_1: XhoI; Site_2:

                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:5427056"
                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:9606"
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     0
     Score 103.8; DB 4;
Pred. No. 3.3e-18;
0; Mismatches 327;
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IMAGE:5427056 5',
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     Gaps
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AL656223.2 GI:
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Croning,M.D.R., Ashurst,J.L., Taylor,R., Zo Sanger Xenopus tropicalis EST project 2001

Unpublished (2003)

On Dec 13, 2001 this sequence version repla

Contact: Huckle E
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
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AL656223 XGC-neurula
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Silurana.
                                                                             Sanger Institute
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FEATURES
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CDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
ECORI-NotI cut cDNA was then ligated into pCS107 with ECORI at
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site 2: NotI
Host: Escherichia coli DH10B
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu035007.plkSp6
Sequencing primer: SP6.
Location/Qualifiers
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/lab_host="Escherichia coli DH10B"
/clone_lib="XGC-neurula"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
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SUMMARIES

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Sugimoto M,

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The present sequence represents the Brevibacterium lactofermentum sucrose PTS (phosphoenolpyruvate:carbohydrate phosphotransferase system or phosphoenolpyruvate-sugar transport system) enzyme II, which has sucrose-binding activity. A coryneform bacteria produced with the sucrose PTS enzyme II gene can have more efficient sugar uptake, and improved aminoacid and nucleic acid productivity. The sucrose PTS gene and it's acid productivity. The sucrose PTS gene and it's disrupted gene, such as one without the sucrose PTS function, can be used to produce new breeds of coryneform bacterial strains to uptake sugar more efficiently e.g. glucose only or and sucrose, and can have improved

Gene encoding sucrose phosphoenolpyruvate-sugar transport system enzyme II obtained by cassette ligation-mediated amplification of downstream domain of coryneform bacterium sucrase gene, with sucrose-binding

Claim 1; Page 29-32; 45pp; Japanese

activity

822.5 24.6 63.6 5 ABB54803 812 24.3 483 7 AB066501 802.5 24.0 63.4 7 AD066501 802.5 24.0 63.4 7 AD066501 801.5 24.0 61.2 6 ABU45919 799.5 23.9 61.2 6 ABU45919 799.5 23.9 61.2 6 ABB28036 791. 23.7 62.2 5 ABP28036 791. 23.7 62.2 5 ABP28055 785.5 23.5 62.0 5 ABP26854 787.5 22.4 64.0 5 ABB49939 738 22.1 379 6 ABU42285 737 22.1 583 7 AD067184 728 21.8 618 8 ADM61668 725.5 21.7 683 4 AAG93207 725.5 21.7 683 4 AAB66721 725.5 21.7 683 4 AAB66721 725.5 21.7 683 5 ABB89333 71.9 21.5 494 5 ABB89332 71.8 21.5 494 5 ABB89322 691 20.7 704 4 ADU60962
6.6 636 5 ABB54803 3 483 7 ABC66501 6.34 7 ADF06734 0 612 6 ABUF06734 0 612 6 ABUF0679 9 612 6 ABB781336 9 612 8 ADF46396 6.7 622 5 ABF280755 620 5 ABF280755 5 620 6 ABU42285 1. 379 6 ABU42285 1. 379 6 ABU42285 1. 1 583 7 ADC97184 1. 1 618 8 ADM66968 1. 7 683 4 AAG93207 1. 7 683 4 AAG93207 1. 7 683 4 AAG93222 1. 7 704 4 AAU60962
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ALIGNMENTS

BB 21	SULT 1 B69080 AAB69080 standard; protein; 661 AA.
	AAB69080;
	11-SEP-2003 (revised) 20-APR-2001 (first entry)
	Brevibacterium lactofermentum sucrose PTS enzyme II protein SEQ ID NO:2.
	Brevibacterium lactofermentum; sucrose PTS enzyme II; sucrase; phosphoenolpyruvate:carbohydrate phosphotransferase system; glucose; coryneform bacterium; phosphoenolpyruvate-sugar transport system.
	Corynebacterium glutamicum.
	WO200102584-A1.
	11-JAN-2001.
	30-JUN-2000; 2000WO-JP004348.
	02-JUL-1999; 99JP-00189512.
	(AJIN) AJINOMOTO CO INC.

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RESULT 2
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             Corynebacterium
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Best Local (
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N-PSDB;
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07-APR-2000;
03-AUG-2000;
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Tateishi
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23-AUG-1999;
03-SEP-1999;
03-SEP-1999;
                                                                                                                                                                                                                 The present invention relates to Corynebacteium glutamicum phosphoenolpyruvate: sugar phosphotransferase system (PTS) proteins. The PTS nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria, as the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful fo typing or identifying C. glutamicum or related bacteria, and as marke
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                                                                                            New metabolic pathway genes of Corynebacterium glutamicum for producing fine chemicals, e.g. lipids, (un)saturated fatty acids, vitamins, cofactors or enzymes used in food, feed, cosmetics or pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (e.g. amino acids, vitamins, cofactors, nucleotides and nucleosides, or trehalose). The polynucleotide sequences encoding the MP proteins are useful for producing fine chemicals, particularly organic acids, non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, (un)saturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes. The fine chemicals are useful in the food, animal feed, cosmetic or pharmaceutical industries. ABG80321-ABG80343 represent the C. glutamicum MP proteins of the invention
                27-JUN-2000; 2000WO-IB000973
                                                                         WO200102583-A2
                                                                                                       Corynebacterium
                                                                                                                                 Phosphoenolpyruvate; sugar
                                                                                                                                                             C.glutamicum
                                                                                                                                                                                             09-APR-2001
                                                                                                                                                                                                                                                      AAB66708 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of Corynebacterium glutamicum metabolic pathway (MP) proteins, and the polynucleotide sequences encoding them. The MP proteins are enzymes involved in the metabolism of melecules important for the normal functioning of cell.
                                              11-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                     SGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIK 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIDAPDMVMFLVCAVVTFVIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGALIALFDIKAVALGAAGFLGVV
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                                                                                                                                                                                                                                                                                                                                                AAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPATP
                                                                                                                                                                                                                                                                                                                                                                                                                                               AEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFP
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                                                                                                                                                             phosphoenolpyruvate protein
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                                                                                                     glutamicum
                                                                                                                                                                                                                                                     protein;
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                                                                                                                                   phosphotransferase
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Pred. No. 2.
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                                                                                                                                   system;
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RESULT 6
ADK46609
ID ADK4
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AC ADK4
AC ADK4
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BT 20-M
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DT 20-M
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DE Stree
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AKW Anti

(first entry)

ADK46609

standard;

protein;

20-MAY-2004 Streptococcus

pneumoniae protein,

Seq

ID No

Streptococcus

pneumoniae.

Antibacterial; Gene therapy; Vaccine;

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Best Local Similarity
Matches 359; Conserv
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23-AUG-1999;
03-SEP-1999;
03-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacteium glutamicum nucleic acids encoding phosphoenolpyruvate: sugar phosphotransferase system proteins or their portions, useful fo typing or identifying C. glutamicum or related bacteria, and as marke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                transformation
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                                                                                      LVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVK
                                                                                                        LVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVK
                                                                                                                                                                                                                     KAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFVIAFGAAIAYGLYLVRRNGSIDPDATAA
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    TP 661
                                AGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPA
                                                                                                                                             PVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ
                                                                                                                                                                    PVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQ
                                                                                                                                                                                                      KAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRRNGSIDPDATAA
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                                                                                                                                                                                                                                                                                                                                                                              Conservative
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99US-0150310P.
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99DE-01042097.
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99.2%;
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Pred. No. 2.9e-170;
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12-MAY-1998;
30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and polypeptides. The nucleic acids and proteins are useful for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, such as S. pneumoniae infection. These may also be used for drug screening procedures. The present sequence represents a Streptococcus pneumoniae polypeptide of the invention. Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecules and polypeptides useful for diagnosing preventing and treating pathological conditions resulting from ba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated Streptococcus pneumoniae nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 3124; 301pp; English.
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FDIKAVALGAAGFLGVVSIDAPDMV----
                                                                                                                            GLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIF-ATASMANIAQGAA
                                                                                                                                                                           VLVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDLLAHGLQ
                                                                                                                                                                                                                                                                                                      IPILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFT
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                                                                                                                                                                                                                                                                                                                                                   FQIIVGPGDVDHVFKE---LDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPL
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                                           TVAVGVKTKNPKLKTLAFPAALSAFLGITEPAIFGVNLRFRKPFFLSLIAGAIGGGLASI
                                                                                                 AILSIPFGLGGFLIGGVHQLIVVSGVHHIFNLLEVQLLAADHANPFNAIITAAMTAQGAA
                                                                                                                                                          AFIIGVVGAKFEKAVRKVVPDVIDLLVTPFVTLLVMSILGLFVIGPVFHVVENYILIATK
                                                                                                                                                                                                                    TFRVFGGNPAVGIVLGMMLVSGSLPNAWAVA---QGGEVTAMNFFGF-IPVVGLQGSVLP
                                                                                                                                                                                                                                             ATKRFGGNEFLGAGIGMAMVFPTLVNGYDVAATMTAGEMPMWSLFGLDVAQAGYQGTVLF
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                                                                      CLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGALIAL
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98US-0085131P.
98US-00107433.
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               -MFLVCAVVTFVIAFGAAIAYGLYLVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     245;
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                                                                              The invention relates to an isolated nucleic acid comprising a sequence encoding a Streptococcus pneumoniae ADR9136polypeptide, or its fragments, with any of 9 fully defined sequences (appearing as ADR94308, ADR94499, ADR94800, ADR94837, ADR94969, ADR95253, ADR95642, ADR95682, ADR946079) or any of the fully defined sequences appearing as ADR91705, ADR91886, ADR92197, ADR92234, ADR93039, ADR93079, ADR92366, ADR92650 or ADR93186, ADR92197, ADR923234, ADR93039, ADR93079, ADR92366, ADR92650 or ADR93186 or at least 20 or 30 consecutive nucleotides of the nucleotide sequences, or at least 40, 60 or 300 consecutive nucleotides, which is hybridisable under high stringency conditions to the nucleotide sequences. The nucleic acids and proteins are chosen from 5206 disclosed sequences. Also included are a recombinant expression vector comprising the isolated nucleic acid cited above operably linked to a transcription regulatory.
sequences as cited above. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment o pathological conditions resulting from bacterial infection by
                                                  element, a cell comprising the recombinant expression vector and a probe comprising at least 20 consecutive nucleotides of the nucleotide
                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid encoding a Streptococcus pneumoniae polypeptide, useful for diagnosing, preventing and/or treating pathological conditions resulting from the bacterial infection
                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3250; 151pp; English.
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12-MAY-1998;
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Best Local Simi
Matches 223;
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 Enterococcus faecalis infection; transcription regulatory element;
                                  Enterococcus
                                                                   22-APR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       producing an E. faecalis polypeptide, an isolated nucleic acid comprising a sequence not given in the specification, a recombinant vector comprising the nucleic acid and a cell comprising the recombinant vector. The polynucleotides can be used to detect the presence of E. faecalis in a sample. The sequences are useful for preparing a composition for diagnosing or treating Enterococcus faecalis infection. This sequence represents an E. faecalis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to Enterococcus faecalis polynucleotides and polypeptides. The invention also relates to a recombinant expression vector comprising a polynucleotide operably linked to a transcription regulatory element, a cell comprising a recombinant vector, a method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid comprising a sequence encoding polypeptide, useful for preparing a composition treating E. fecalis infection.
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N-PSDB; ADH84532.
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                                                                  SVTFAITYFYG--RTRSSSIFAAEAIAEQTSVDTSEINTNQIANADEPTTVETIVSPLAG
                                                                                                VIAFGAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTI--IQAPLTG
                                                                                                                                                                                                    WTNGIGHGDFIFVVASMANVAQGAATFAIWFLTKNSKTKSLASSAGLSALLGITEPALFG
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EITTLGSVNDPVFSSESIGKGIAIKPNGNTIYSPVDGIVQVVFETGHAYDLKS----NTG
                             EAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSN
                                                                                                                                   VNLKYRFPFFCALIGSGIAAAITGLLKVVAVSLGSAGFLGFLSINATSIPFYLLCELISF
                                                                                                                                                                 VNLRLRWPFYIGIGTAAIGGALIALFDIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTF
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                                                                                                 The present invention relates to the genome sequence of Listeria CC monocytogenes ECD-e (see ABA0341). The genome sequence and fragments of CC it are useful for selecting probes and primers for detecting genes in L. CC monocytogenes and related organisms, and for studying genetic CC polymorphisms and other genomes. The present sequence is a protein CC encoded by the genome sequence of the present invention. Proteins CC expressed from the genome sequence are useful for raising specific CC antibodies, identification of L. monocytogenes and related organisms, and CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin CC B12. The genome sequence and proteins encoded by it are also useful for CC selecting compounds that regulate gene expression and cell replication CC and modulate L. monocytogenes related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and CC waccines compositions for the treatment or prevention of infections by L. CC monocytogenes and related organisms. Note: The sequence data for this CC patent did not form at of the printed specification, but was obtained CC in electronic format directly from WIPO at
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dussurget C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Dlaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H;
                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and relat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
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, Glaser P, Kunst F, Cossart
M, Ng E, Vazquez-Boland JA;
 DB 5;
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25-OCT-2001;
08-FEB-2002;
                                                                                      21-MAR-2002;
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                                                                                                                                                              Listeria monocytogenes
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         2001US-00815242.
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the 6213 antisense sequences given in the specification where expression (C) of the nucleic acid inhibits proliferation of a cell. Also included are: (C) a vector comprising a promoter operably linked to the nucleic acid (C) encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated (C) polypeptide or its fragment whose expression is inhibited by the nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway (C) identifying a compound that influences the activity of identifying a compound that influences the activity of a gene product or that has an activity against a biological pathway (8) identifying a compound that influences the activity of identifying a compound that influences the activity of a gene product or a gene on which a proliferation or that inhibits groliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational control did not form post of the nitrated specification, but was obtained this interest prokaryotic essential genes. Note: The sequence data for this chained
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Matches 225
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296 LQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIEL-ELFNQGGSFIFATASMANIAQG
                                                                                                                        236 LPVLVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDLLAHG
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Trawick JD,
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                                                               IPIILAVWFLSILERFLNSKIHEAAKTFLTPMICLMLIVPLTFLAFGPLGTFISQGLASG
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Pred. No. 1.9e-85;
4; Mismatches 228;
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Forsyth
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Xu HH;
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                    The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also pseudomonas aeruginosa and Enterococcus faecalis. The invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense; prokaryotic cellular proliferation antibacterial; drug design.
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                                                                                                                                                                                                                                                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611495/70.
N-PSDB; AAS55733.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto
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2000US-0207727P.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATKREGGNEELGAGIGMAMVEPTLVNGYDVAATMTAGEMPMWSLEGLDVAQAGYQGTVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPVIVATGLEMGVRGLENALEM------PLPGDFATYTQILTDTAFIILPGLVVWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQIIVGPGDVDHVFKE---LDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPL
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GDAVIEV
                                                                                                             FEAKVAQGNKVKAGDVLGTFDSNKIAAAGLDDTTMVIVTNTADYASVAPVAT---GSVSK
                                                                                                                                                                                                                                                                                                                                      --EDEVDATAAAKQAEVAEEKEEVAPAALQNETLV--TPIVGDVVALADVNDPVFSSGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDIKAVALGAAGFLGVVSIDAPDMV------MFLVCAVVTFVIAFGAAIAYGLYLVRR
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33.3%;
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Pred. No. 2.5e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246;
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AQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGMFQIIVG

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Similarity

28.4%; ilarity 34.9%; Conservative 128

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Score 949; DB 6; Pred. No. 1.3e-84; 8; Mismatches 253

Length 655;

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CC identity to any of the 2469 amino acid sequences, identified in the CC specification (available on a computer readable format), or its fragment, CC expressed from 2469 of 2489 identified by Acoding regions from the CC Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC hass6454. Also included are an antibody which binds one of the proteins, CC treating a patient by administering the protein, DNA or antibody (in a CC composition), a kit comprising first and second primers, which are the CC sequence contained within a Streptococcus muclectides 8-100 of a CC sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus mucleic acid sequence, where CC the first primer is substantially complementary to the target sequence contained within a Streptococcus mucleic acid sequence, where CC the target sequence, and where the parts of the primers having CC substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the CC protein, and determining whether the test compound binds to the protein CC and a Streptococcus pneumoniae bacterium, where one or more genes cc encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for CC treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis medica or ear infection. They are also useful in developing vaccines, cd diagnostics and antibiotics. The methods are useful as medicaments for CC diagnostics and antibiotics. The methods are useful as 2469 proteins CC expressed by the identified coding regions from the genomic sequence. CC Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from MIPO CC at fig. 12 contains the sequence of the composition of the printed CC specification as obtained in ele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media ear infection.
Sequence 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacterial meningitis; pneumonia;
antiinflammatory; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a protein comprising or having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 3912; 56pp; English.
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immunostimulant; audit
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18-APR-2001;
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                                                                   2001US-0283948P.
2001US-0284443P.
                                                                                                                                       2002WO-US011524
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                        pneumoniae; infection; otitis media; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                pneumoniae polypeptide
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Streptococcus pneumoniae polynucleotides, useful preventing S. pneumoniae infections, or non-systemic otitis media, which are induced or exacerbated by S.
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Wooters JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity and are useful in gene therapy
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DB; ABZ42306.
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234; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     VFAYYEMHRHDEREAQVSLPATISAYLGVTEPALFGVNVKYIYPEVAGMTGSALAGMLSV
                                                                                                                                                                                                                                                                                                                                                                                                                            CLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLTGPVKWLFGAIFGALYAPFVITGLHHMTNAIDTQLIADAGGTALWPMIALSNIAQGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G--GPVG---GLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFATASMANIAQGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSLSYLEIFWHKHIPEVISMIFVPFLSLIPALILAHTVLGP----IGWTIGQGLSSVVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEFLGAGIGMAMVFPTLVNGYDVAATMTAGEMP--MWSLFGLDVAQAGYQGTVLPVLVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               655 AA;
                              GLDGKGFESLVVQGDHVTVGQQLIRFDMDVIKAAGLVTETPVIITNQDAYTATIP-GTYP
                                                                     NLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYG
                                                                                                                                           FASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTV
                                                                                                                                                                                                                                                                                                 TPNVTAASIGIGGLPGILSIQPQYMLPFAGTMLVAIVVPMLLTF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDLLAHGLQGLYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQILGIVLGICLVSPQLLNAYAVASTPAADIAANWVWNFGYFTVNRIGYQAQVIPALLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILGFRNVLEGVHWSMLDGKTITESSOFWAGVNHFLWLPGEAIFOFLFVGITWSVSRKNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMAINNVL--VAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTATKRFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NDVPIFYNDF-TAVSGIEGVSKEAAKSAAKSNONVVQGVMTTLAEIFTPIIPALIVGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGDVDHVFKELDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPLIPILVGGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AORILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGMFQIIVG
                                                                                                                  FASGVMGQGLVIEPSQGELTSPVNGTVTVLFPTKHAIGI--VSDEG-
                                                                                                                                                                                                        FTK-----TEGDTNLQAEFVAQEEAEFVNHEPVELTSVEIISPLTGQVKELSQATDPI
                                                                                                                                                                                                                                                  IDPDATAAPVPAGTTKAEAE----APAEFSNDSTI-----IQAPLTGEAIALSSVSDAM
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Pred. No. 1.3e-84;
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-VELLIHIGMDTV

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640

581 525 ---FFRKAGL

521 472 471 421 415 361 356 301 302 245

Length Indels

56;

Gaps

19

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LGEIEAGANLL

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RESULT 14
ABP27216
ID ABP27
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                                                                                                                                                           CC The invention relates to a protein (ABP25413-ABP30895) from group B CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in CC the specification. The proteins have antibacterial and antiinflammatory CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and CC antibodies that bind (I) are used in the manufacture of medicaments for CC the treatment or prevention of infection or disease caused by CC Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. CC Nucleic acids encoding (I) are used to detect Streptococcus in a CC biological sample. (I) is used to detect Streptococcus in a CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by CC used as a vaccine or diagnostic composition. The disease caused by CC streptococcus that is prevented or treated may be meningitis. Nucleic CC acid encoding (I) may be used to gene therapy. Antibodies to (I) are used for affinity CC ctromatography, immunoassays, and distinguishing/identifying
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Best Local S
Matches 226
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                                                                                                                       Sequence
                                                                                                                                        chromatography, immunications
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 3514; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pyogenes.
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                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus protein for the treatment or ease caused by Streptococcus bacteria, such ecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-352536/38
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INST GENOMIC RES
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Masignani
                                                            Conservative
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                                                          28.0%; Score 935.5;
34.7%; Pred. No. 2.6e
tive 108; Mismatches
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                                                          5; DB 5;
2.6e-83;
nes 273;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevention of infection or as meningitis, and for
                                                            Indels
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RESULT 15
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         WPI; 2004-212399/20.
N-PSDB; ADK43782.
                                                                                                                  02-JUL-1997;
12-MAY-1998;
                                                                                                                                                         26-MAY-2000; 2000US-00583110.
                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                         Streptococcus
                                                                                                                                                                                                                                                                                                                     20-MAY-2004
                                                                                                                                                                                                                                                                                                                                              ADK46443;
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                                                  Doucette-Stamm
                                                                                                     30-JUN-1998;
                                                                                                                                                                                   02-MAR-2004.
                                                                                                                                                                                                            US6699703-B1
                                                                                                                                                                                                                                                              Antibacterial; Gene therapy; Vaccine; Streptococcus
                                                                           (GENO-) GENOME THERAPEUTICS CORP
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LENGTH: 627
TYPE: PRT
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Nucleic Acid and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT FILING DATE: 0000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR PHILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
                                                                                                                                                  166
                                                                                                                                                                                                                                                                        118 IPILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFT
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ATKREGGNEFLGAGIGMAMVEPTLVNGYDVAATMTAGEMPMWSLEGLDVAQAGVQGTVLP
                                                                                                                                                                                                                                                                                                                                            FQIIVGPGDVDHVFKE---LDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPL 117
                                                                                                                                                                                                                                     IPVIVATGLEMGVRGLENALEM------PLPGDFATYTQILTDTAFIILPGLVVWS
                                                                                                                                                                                                                                                                                                                      YOIIFGTGTVNKMYDEVVVLGLPTS----SKDDMKAEVAKQGNWFQRAIRTFGDVFVPI
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                                                                 AFIIGVVGAKFEKAVRKVVPDVIDLLVTPFVTLLVMSILGLFVIGPVFHVVENYILIATK
                                                                                                      VLVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDLLAHGLQ
                                                                                                                                                  TFRVFGGNPAVGIVLGMMLVSGSLPNAWAVA---QGGEVTAMNFFGF-IPVVGLQGSVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.9%; Scilarity 33.4%; Pr
Conservative 141;
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Pred. No. 2.
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76 60

131

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RESULT 2
US-09-107-433-3250
US-09-107-433-3250
; Sequence 3250, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   망
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                                                                                                                                                   TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3250:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

RECISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007
                                 MOLECULE TYPE: protein HYPOTHETICAL; YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: NO. 107,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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                                                                                              LENGTH: 643 amino acids TYPE: amino acid TOPOLOGY: linear
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           ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
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Sequence 5822, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1997-08-15
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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LOCATION: (B) LOCATION 1...643
SEQUENCE DESCRIPTION: SEQ ID NO: 3250:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                             GANLLINV 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQGIAVKPSQGVVYAPADAEVSIAFPTGHAFGLKTR----NGAEVLIHVGIDTVSMNGDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AILSIPFGLGGFLIGGVHQLIVVSGVHHIFNLLEVQLLAADHANPFNAIITAAMTAQGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDLLAHGLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                    FEAKVAQGNKVKAGDVLGTFDSNKIAAAGLDDTTMVIVTNTADYASVAPVAT---GSVAK 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EGLAGTGNGITIIPGTMLYVGNGQLPQYLLMVAVSFALGFALTYMFGY-----
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33.4%; Pred. No. 3e-90;
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644

577 587 521 527 465 468

417

297 297 237

3.9e-87;

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FILE REFERENCE: PATHO0-OTA
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR PILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 2958
LENGTH: 655
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-583-110-2958
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US-09-583-110-2958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin
SEQ ID NO 5822
LENGTH: 496
                                                                                                                                                                                                                                                                                                         Sequence 2958, Application US/09583110 Patent No. 6699703
     Query Match
                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 208; Conserv
                                                                                                                                                                                                                                         APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating
TITLE OF INVENTION: Programminate for Diagnostics and Therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                           628
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    Score
  935;
    DB
    4
Length 655;
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US-09-107-532A-5288
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Matches 229; Conservative 133;
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 SOFTWARE: ASCII
                                                                                                                   CITY: Waltham
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Sequence 5288, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCCOCCUS
                                COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 LFDIKAVALGAAGFLGVVSIDAPDMVMF----LVCAVVTFVIAFGAAIAYGLYLVRRNG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCQCLVIEPSQCELTSPVNGTVTVLFPTKHAIGI--VSDEG--VELLIHIGMDTVGLDGK
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COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGT 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFNVTAASIGIGGLPGILSIQPQYMLPFAGTMLVAIVVPMLLTF-----FFRKAGL
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AKDLLQAIGGKENVTAVTHCATRMRFVLRDDKKANVKAIESIPAVKGTFTNAGQFQVIIG
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                                                                                                                                                                                                                                                                                                                                                 and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                 CORPORATION
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Best Local
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NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: (B) LOCATION 1...628 SEQUENCE DESCRIPTION: SEQ ID NO: 5288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL; YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATION FOR SEQ ID NO: 5288: SEQUENCE CHARACTERISTICS:
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511
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                      AIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPL 591
                                                                                                               IDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGV
                                                                                                                                                       GVKAFSSSLVSLLTIPTFINTVDGVESNVTVAVIATGIAFVLAFVGTLILGFDEQTQDNQ
                                                                                                                                                                                            DIKAVA-----LGAAGFLGVVSIDAPDMVMFLVCAVVTFVIAFGAAIAYGLYLVRRNGS
                                                                                                                                                                                                                                                                                                               IYGFSPIVAGLIMGSLWQVFVMFGMHWGFVPIMFLNIEQYGFDVLMPMLLPAILAQGGAA
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AIDPEVGELVAPADGEITTIFFTGHAVGITT--TDGA--EILIHIGMDTVELNGNGFEIL
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                                                                            --NKHANAGEPITSARHTLKSPLTGKVLPLSEVPDQVFSSGVMGKGI
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US-09-489-039A-8212
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8212
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIEULA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Klebsiella pneumoniae
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                                                                                                                                                                                            DIKAVALGAAGFLGVVSIDAP---DMVMF--LVCAVVTFVIAFGAAIAYGLYLVRRNGSI 472
                                                                                                                                                                                                                                    IYAFAPWLAGAVLGAMWQVCVIFGLHWGLVPLMINNMTVLGHDSMLPIILPAVIAQVGAV
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  IIPAVĠQVIAPFPGEVASLFQTKHAIGL----QSDSGIELLIHVGIDTVKLDGVPFTAHV
                                    IVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLK
                                                                                                                 DPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVA
                                                                                                                                                       NSYAYSFGLPNIFFPAQMIPPGGIDASVWGGLIGTGVAFVLACVLTFFAGL------
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32.7%; Pred. No. 5.4e-81;
tive 124; Mismatches 271
                                                                              -GAVTVAPAS-AND---ILAPMSGSVIALEQVPDSTFASGLLGKGVA
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Length Indels

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KQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVA

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RESULT 7
US-09-134-000C-4606
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 VGDLLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGGSFIFATAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 IIVGPGDVDHVFKELDDATSKDIAVSTEQL---KDVVANNANWFSRAVKVLADIFVPLIP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 YHELAEKIVKNVGGQENINSLTHCITRLRFKLKDESQANDDVLKNMDGVVTVMKSGGQYQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201; Conservative 132; Mismatches 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 HKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGMFQ
LNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEI 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GANYTSSVVPIIFIIAFAAQVQKVFKRIIPEVVQTFLVPFFVLLIALPIGFLVIGPIVSM 322
                                                                      ANGALGNGVVIEPTEGKVVAPFDGTIVTLFPTKHALGLIS----DNGTELLIHIGIDTVQ
                                                                                                                                                                                                                           LYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMF
                                                                                                                                                                                                                                                                                                                              AAIGGALIALFDIKAVALGAAGFLGVVSI----DAPDMVMFLVCAVVTFVIAFGAAIAYG 462
                                                                                                                                                                                                                                                                                                                                                                                FAASFAQTAVVLAMFFKLKDKKLKALCPPAIISGIFGVTEPAIYGITLPKKWPFIYSMIG 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTDLLSAGFTALMSFSPALYGLILGFFWQVLVIFGLHWSVVPLAIMQVTQEGSSQVLTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAGYQGTVLPVLVVSWILATIEKFLHXRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKÉRLHPMVGIVÍGAÁLCYPTIQGSALQTÁFETTAGÁGAAAPYNLFGLPAYNTFMGIPWV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALAAAGMVKGLNALLV-----FLKLYTATSGTYTMLNGIGDAIFYFMPVILGYTAA 202
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                                                                                                                                                                            -FFFWKDNTVEEEEVI--IDKTTIKKEN-----ITSPVKGRVLSLKNAEDPAF
                                                                                                                                                                                                                                                                               GAVGGLYLMINNVTAYTMGGLGIFGVLNFINGDDASGMIQSFIAIAIAAVVGFGLT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRFGGNEFLGAGIGMAMVFPTLVNGYDVAA---TMTAGEMPMWSLFGLDV------A 227
                                                                                                                          ASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVN 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEGDRVQAGDLLIEFDRQAILDAGYDLVTPIIISNSDDYREIDTVASSAVEAGQPLLSVS 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.6%; Score 855; DB 4; Length 670; 30.1%; Pred. No. 7.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACID SEQUENCES RELATING TO FOR DIAGNOSTICS AND THERAPEUTICS
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US-09-107-532A-3902
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                                                                                                                                                                                                                                                                         Matches 196;
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3902:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...631
SEQUENCE DESCRIPTION: SEQ ID NO: 3902:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD/RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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138
                                          115
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                                                                                                                                    61
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APTLGVLAGSGLIKGVLALCTSLNLLTTE----
                                          VPLIPILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLV 174
                                                                                                                                  FQIIVGPGDVDHVFKELDDATSKDIAVSTEQLKDVVANNANWFSRA-----VKVLADIF 114
                                                                                                                                                                               MDYSQLAKDIVRFVGGEENVSNVYHCATRLRFTLKDNKKADKEKVEQLEGVITVVEAGGM
                                                                                                                                                                                                           MDHKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM
                                                                                       FQVVVG-----NAVNEVYDVLSKQM-----KLEDDASSGKRGTEKKGILNSFIDMIAAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 631 amino acids
                                                                                                                                                                                                                                                                    24.7%; Score 826; DB 4; ilarity 30.5%; Pred. No. 6.5e-76; Conservative 123; Mismatches 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD/ROM ISO9660
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                         243;
SGTYIILNAAADAFFYFLPIFL 188
                                                                                                                                                                                                                                                                                                               Length 631;
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RESULT 9
US-09-489-039A-13018
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US-09-489-039A-13018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13018
LENGTH: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13018, Application Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                       Matches 175;
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
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                                                                                                                        LVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTATK
                                                                                                                                                                  MQIIFGTGVVNKVYAAFIQAAGISES-SKSEAADLAGKKLNPFQRIARLLSNIFVPIIPA
                                                                                                                                                                                                       FQIIVGPGDVDHVFKELDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPLIPI 120
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                                     RFGGNEFLGAGIGMAMVFFTLVNGYDVAA---TMTAGEMPMWSLFGLDVAQAGYQGTVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYFQSAVSDGKKVRKGDLLMEVDLQELIKEGYDPTTMVIVTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNG
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EFGGNPYLGATLGGILTHPALTNAWGVAAGFHTM----NFFGIEVAMIGYQGTVFP
                                                                                 IVASGLIMGLIGMVKTYGWVDPSNALYI-----
                                                                                                                                                                                                                                                   MDFEQISRSLLPLLGGKENIASAAHCATRLRLVLVDDALADQQAIGKIDGVKGCFRNAGQ
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                                                                                                                                                                                                                                                                                                                              24.3%;
ilarity 37.6%;
Conservative 88
                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae
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                                                                                                                                                                                                                                                                                                                                       88; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                           Score 812; DB 4;
Pred. No. 1.1e-74;
                                                                               - MLDMCSSAAFIILPILIGFTAAR
                                                                                                                                                                                                                                                                                                                                                                              Length 483;
                                                                                                                                                                                                                                                                                                                                     Indels
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TITLE OF INVENTION: DIAGNOSTICS AND THERAPEU
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7019
LENGTH: 634
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US-09-543-681A-7019
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APPLICANT: GARY BRETON
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nes 211; Conserv
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MIGGAIAGLFAGIVKLKAFVYVTPGLLSLPMWIS-DTDNQV---VNAIITLLIASVATFI
                                                                                                           ANIAQGAACLAVFFLAKSEKLKGLAGASGVSAVL-GITEPAIFGVNLRLRWPFYIGIGTA 407
                                                                                                                                                                                                          LLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQGG---SFIFATASM
                                                                                                                                                                                                                                                      PVFIGFSAAKIFNCNQYLAAMVCLAMVSP-----EWTSLVKAGE-PV-EFMHIPVALVK
                                                                                                                                                                                                                                                                                                                                                                            PVLVGFTATKRFGGNEFLGAGIGMAMVFPTLVNGYDVAATMTAGEMPMWSLFGLDVAQAG
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                                       AIGGALIALF----DIKAVALGAAGFLGV---VSIDAPDMVMFLVCAVVTFVIAFGAAIA 460
                                                                                   SNMSQAAASLAVSVRTKNKTLKQLAFSASITAFFGGITEPAMYGVNLKLKKPMY----AC
                                                                                                                                                                                                                                                                                             YQGTVLPVLVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGD
                                                                                                                                                                                                                                                                                                                                                                                                                          TGSIAPVIPLLAGAGMGKVLLIVL-----TMLGWLDKSDQTYYILNFIFNTAFYFM
                                                                                                                                                                    LIADGVILIQEHTGFIAIPLLVAIYPWLVSIGMHKALSPVSIMLVEQKGFDPIIRVMALC
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; ORGANISM: Streptococcus pneumoniae US-09-583-110-2911
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US-09-583-110-2911
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SEQ ID NO 2911
LENGTH: 612
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acid and Amii TITLE OF INVENTION: Pneumoniae for Diagno FILE REFERNCE: PATHOO-07A CURRENT APPLICATION NUMBER: US/09/583,110 CURRENT FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US 09/107,433 PRIOR PILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-05-12 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1997-07-02
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                                                                                                                                                                                                                                                                                                                                                                                   ATKREGGNEFLGAGIGMAMVEPTLVNGYDVAATMTAGEMEMWSLEGLDVAQAGYQGTVLP
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-- AAMIGGGLAGLFAGLTSVKAYLFAVPSLIALPQFIYSDVPSNIVNALIVAVISVVITF
                                        IGTAAIGGALIALF----DIKAVALGAAGFLGV---VSIDAP-DMVMFLVCAVVTFVIAF
                                                                                  AMLGSNLAQGAASMAVALKSKNNNTKQIAFAAGFSALLAGITEPALYGVTLKYKKPLY--
                                                                                                                                                                   QMYGVAGWLTLAILGAIMPFIVMTGWHWAFAP-----IFLAASIATPDVLILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQIIVGPGDVDHVFKE---LDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPL 117
                                                                                                                           ----NIAQGAACLAVFFLAKSEKLKGLAGASGVSAVL-GITEPAIFGVNLRLRWPFYIG
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VENTION: Nucleic Acid and Amino Acid Sequences Relating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.8%; Score 796.5; DB 4; ilarity 31.4%; Pred. No. 6.9e-73; Conservative 118; Mismatches 238;
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RESULT 12
US-09-107-532A-6811
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                   Query Match
Best Local
                                                                                 Matches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6811: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    NAME/KEY: misc feature LOCATION: (B) LOCATION 1... SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Den
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    FEATURE:
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479 DVQDKTFSDKLIGDGVAIIPSEGKVYAPFDGKITNIFPTKHAIGL--KSDEG--VELLIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 GAAIAYGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALS
                                   87 VSTEQLKDVVANNANWFSRAVKVLADIFVPLIPILVGGGLLMAINNVLVA---QDLFGPQ 143
  7
                                                                                                     Similarity
VSTEQGKAAAKQNLHPVQRAIAVLAEIFTPLIPAIIVGGLILGFRNVLEGIQFESLGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGLDTVELKGQGFISHVEEGDRVFKNQLIFEMDLNLIKTKGYETVTPVIVTN
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                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus
                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/107,532A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 583 amino acids
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                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pamela Deneke
                                                                               Score 737; DB 4;
Pred. No. 8.8e-67;
L9; Mismatches 239
                                                                                                                                                                                    .583
: 6811:
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                    Length 583;
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RESULT 13
US-09-107-433-5169
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Patent No. 6800744
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
AITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                   APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: JULY 2, 1997
ATTORNEY, AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,433 FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5206 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYSVAST-AAADIPFWDFGFAQVQMIGYQAQVIPAMLAGFMLAYLBIFFRKYIPQSISMI 183
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                                                                                                                                                                                                                                                                                  COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
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     TELEPHONE:
                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                         <Unknown>
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NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5156
LENGTH: 481
                                                                                                                                                                                          Sequence 5156, Application US/09543681A PATENT NO. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 168;
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                                                        TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: DIAGNOSTICS AND THERAL FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
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INFORMATION FOR SEQ ID NO: 5169:
SEQUENCE CHARACTERISTICS:
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LOCATION: (B) LOCATION 1...!
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAHGLQGLYDFG---GPVG---GLLFGLVYSPIVITGLHQSFPPIELELF-NQGGSFIFAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QATDPVFASGVMGQGLVIEPSQGELTSPVNGTVTVLFPTKHAIGI--VSDEG--VELLIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGLYLVRRNG---SIDPDATAAPVPAGTTKAE--AEAPAEFSNDSTIIQAPLTGEAIALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASMANIAQGAACLAVEFLAKSEKLKG-LAGASGVSAVLGITEPAIFGVNLRLRWPFYIGI 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGTVLPVLVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDL
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(B) LOCATION 1...530
SEO ID NO: 5169:
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Pred. No. 9.2e-61;
1; Mismatches 184
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                                                                                                                                                       AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL AND THERAPEUTICS
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US-09-107-532A-6004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6004, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                             SOFTWARE: ASCII
CURRENT APPLICATION NUMBER: US/09/107,532A
APPLICATION NUMBER: US/09/107,532A
                                                                                        FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID ENTEROCOCCUS
                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 GIGVGGLPGILSIQPTYWLVYLLAMIVAIVVPIGLTILVYRY-KEKAGTLQVD
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                                                       APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
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NAME: Ariniello, Pamela Den
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                     OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                      CITY: Waltham
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                   Pamela Deneke
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AND AMINO ACID SEQUENCES
FAECIUM FOR DIAGNOSTICS P
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...590
SEQUENCE DESCRIPTION: SEQ ID NO: 6004:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
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      574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FATDILMAGFETLLALSPVIYGAIVGFFWQILVMFGLHWAIVPMGLMQFSVNGWQNIMTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GYQGTVLPVLVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMR 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTATK 180
                                         DTVNLNGTHENPLKKQG 595
                                                                                 DAAFAQGTLGRGILIYPEKGEVRAPFDGTVMTLFPTKQAIGMVSE----TGLELLIHVGL
                                                                                                                      DAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGF 578
                                                                                                                                                                                                                                                                                 TAAIGGALIALFDIKAVALGAAGFLGVVSI-----DAPDMVMFLVCAVVTFVIAFGAAIA
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DTVQLEGKYFESLVQQG
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                                                                                                                                                                                                  YGLYLVRRNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDS--TIIQAPLTGEAIALSSVS
                                                                                                                                                                                                                                             GGALGGAYSGLMNLTSWNQGGLGIFTIPNYIRPDGDLTDVINVLIGIAIAMVVSFTLTFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 590 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.3%; Score 644; DB 4; Length 590
26.6%; Pred. No. 3.6e-57;
Ltive 130; Mismatches 249; Indels
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Search completed: March Job time: 46 secs

7,

2005,

21:57:09

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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949
801.5
799.5
785.5
738
            725.5
725.5
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1: /cgn2=6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2=6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2=6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

6: /cgn2=6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

6: /cgn2=6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

7: /cgn2=6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

9: /cgn2=6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2=6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

10: /cgn2=6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2=6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

12: /cgn2=6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

13: /cgn2=6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

14: /cgn2=6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

15: /cgn2=6/ptodata/1/pubpaa/US10B PUBCOMB.pep:*

16: /cgn2=6/ptodata/1/pubpaa/US10D PUBCOMB.pep:*

16: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

17: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

18: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

19: /cgn2=6/ptodata/1/pubpaa/US10 PUBCOMB.pep:*

19: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

19: /cgn2=6/ptodata/1/pubpaa/US10 PUBCOMB.pep:*
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3342
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Copyright (c) 1993 - 2005 Compugen Ltd.
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15 US-10-282-122A-60875

15 US-09-815-242-13467

15 US-09-815-242-13467

16 US-10-474-776-375

17 US-10-472-928-3912

18 US-10-282-122A-73843

18 US-10-282-122A-73843

19 US-10-282-122A-7439

19 US-10-282-122A-70209
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Sequence 6404, Appl
Sequence 10, Appl
Sequence 60875, A
Sequence 3315, Appl
Sequence 375, Appl
Sequence 73843, A
Sequence 1038, Ap
Sequence 1038, Ap
Sequence 70209, A
Sequence 6961, Ap
Sequence 6661, Appl
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249	477	483	485	482	474	474	476	480	454	545	403	439	450	526	466	454	454	474	484	484	484	334	453	455	429	484	484	453	381	451
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0-4/4-//6-36	-10-282-122A-6	-10-282	-10-282-122A-4	-10-282-122A-769	-282-122A-5663	US-09-815-242-10243	-10-282-122A-673	10-282-122A-6015	10-282-122A-4563	-10-156-761-114	282-122A-52	09-815-242-566	-10-282-122A-7	282-122A-5	-10-282-122A-5	-10-282-122A-6	-10-282	US-10-282-122A-70588	US-10-470-048B-229	US-10-282-122A-44138	US-09-815-242-12272	US-10-472-928-3552	US-10-282-122A-55853	US-09-815-242-13794	US-10-282-122A-73368	US-10-282-122A-56917	US-09-815-242-10809	US-10-282-122A-75796	-474-	-10-282-122
Sequence 3554, App Sequence 3554, Ap	e 60299	e 56083,	ø	e 76983,	æ	Sequence 10243, A	e 67341,	Sequence 60159, A	45636,			5			e 53222,			e 70588	Ф	æ	12272,	æ	æ	13794	æ	Sequence 56917, A	_	Ф	367,	Sequence 57628, A

ALIGNMENTS

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APPLICANT: IKEDA, MASATO

APPLICANT: OZAKI, AKIO

ITITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626

CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: UP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/280988

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOPTWARE: PATENTING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOPTWARE: PATENTING SET NOS: 7059

SOPTWARE: PATENTING SET NOS: 7059

SEQ ID NO 6404

LENGTH: 661
                                                                                                   ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6404, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
Query Match 99.0%;
Best Local Similarity 98.9%;
Matches 654; Conservative 4
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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ANDO, SEIKO
  Score 3310; DB 9;
Pred. No. 2.1e-276;
4; Mismatches 3;
                                                Length 661;
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                                                                                                                                                                                                                Sequence 10, Application US/10450055
Publication No. US20040043953A1
GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
TITLE OF INVENTION: No. US20040043953A1el genes
FILE REFERENCE: 936_2000
                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/450,055
CURRENT FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VETS. 2.0
SEQ ID NO 10
                                      Query Match
Best Local Similarity
                             Matches
                                                                                     LENGTH: 468
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
-10-450-055-10
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                            Conservative
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                                         69.8%;
                            4;
                         Score 2332; DB 15;
Pred. No. 3e-192;
4; Mismatches 3;
                                                                                                                                                                                                                             of Corynebacterium
                                                     Length 468;
                            Indels
                          <u>,</u>
                          Gaps
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TITLE OF INVENTION: Identification of Essential Genes in FILE REFERENCE: ELITEA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-09-6
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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OR FILING DATE: 2000-11-27

OR APPLICATION NUMBER: 60/257,931

DR FILING DATE: 2000-12-22

OR APPLICATION NUMBER: 60/267,636

OR FILING DATE: 2001-02-09

DR APPLICATION NUMBER: 60/269,308

DR APPLICATION NUMBER: 60/269,308

DR APPLICATION NUMBER: 60/269,308

DR FILING DATE: 2001-02-16
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
Wall, Daniel
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US-09-815-242-13467

Sequence 13467, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Karit.

APPLICANT: 2yskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Ess;
TITLE OF INVENTION: Prokaryotes
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NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60875
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60875
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Best Local Similarity
Matches 225; Conser
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No. 1.8e-73;
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NUMBER OF SEQ ID NOS: 14110
SOPTWARE: FastSEQ for Windows V.
SEQ ID NO 13467
LENGTH: 627
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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                                                                                                                                                                     NGSIDPDATAAPVPAGTTKAEAB-APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKL
                                                                                                                                                                                                                                                                                     TVAVGVKTKNPKLKTLAFPAALSAFLGITEPAIFGVNLRFRKPFPLSLIAGAIGGGLASI
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                    FEAKVAQGNKVKAGDVLGTFDSNKIAAAGLDDTTMVIVTNTADYASVAPVAT---
                                                FNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEA
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341 416 401 468 449 356

297 281 60 117 115 177 165

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TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING
TITLE OF INVENTION: ANTICENS AND USES THEREOF
FILE REFERENCE: AM10649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
SEQ ID NO 375
LENGTH: 655
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-10-474-776-375
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Publication No. US20040110181A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 234; Conserv
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                                      GLDGKGFESLVVQGDHVTVGQQLIRFDMDVIKAAGLVTETPVIITNQDAYTATIP-GTYP
                                                                            NLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN---YKKTGPVNTYG
                                                                                                                                                    FASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTV
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                                                                                                                    FASGVMGQGLVIEPSQGELTSPVNGTVTVLFPTKHAIGI--VSDEG--VELLIHIGMDTV
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US-10-472-928-3912
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SEQ ID NO 3912
LENGTH: 655
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CURRENT FILLING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
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APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE!
FILE REFERENCE: P026926WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 4979
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OTHER INFORMATION: PTS system, IIAl OTHER INFORMATION: Cellular location of the INFORMATION: Similar to strater information:
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                                                    FASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTV
                                                                                                                              IDPDATAAPVPAGTTKAEAE----APAEFSNDSTI-----IQAPLTGEAIALSSVSDAM
                                                                                                                                                                      TENVTAASIGIGGLEGILSIQEQYMLEFAGTMLVAIVVEMLLTE-----FFRKAGL
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                      FASGVMGQGLVIEPSQGELTSPVNGTVTVLFPTKHAIGI--VSDEG--VELLIHIGMDTV
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Cellular location: membrane
Similar to strain R6 sequence 15903741 (0.E+01)
                                                                                                  -TEGDTNLQAEFVAQEEAEFVNHEPVELTSVEIISPLTGQVKELSQATDPI
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/27,931
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/267,636
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                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73843
LENGTH: 612
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 205; Conserv
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APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
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                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Streptococcus pneumoniae
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APPLICATION NUMBER: 60/269,308
118 IPILVGGGLLMAINNVLVAQDLFGFQSLVEMFPQISGVAEMINLMASAPFAFLFVLVGFT | | | | | | | | | | | | : : :
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Zyskind, Judith
Wall, Daniel
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Malone, Cheryl
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moto, Robert
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US-10-474-776-253
; Sequence 253, Application No. US200;
; Publication No. US200;
; GENERAL INFORMATION;
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE TITLE OF INVENTION: ANTIGENS AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                             205;
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                                                                                                         IPILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFT 177
                                            ATKREGGNEELGAGIGMAMVEPTLYNGYDVAATMTAGEMPMWSLEGLDVAQAGYQGTVLP
                                                                                                                                                                                                               FQIIVGPGDVDHVFKE---LDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPL
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                                                                                      ÍPAMLGGGMLKVLVIIL-----PMLGILQSDSQTIAFLTFFGDAPYYFLPLLLAYS
                                                                                                                                                                       YOILG-NDVANYYKEFVKLGNFESDSV-----VQGHKGNILERIIEYIAGSMTPI
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    ASOKLKVTSTLAMSVAGVLLHPNFVQ-----MVQSGNPL-SLFGAPVTPASYGSSVVP
                                                                                                                                                                                                                                                                                            MDHKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM
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o. US20040110181A1
                                                                                                                                                                                                                                                                                                                                         23.9%; Score 799.5; DB ilarity 31.4%; Pred. No. 7e-60; Conservative 119; Mismatches 2
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PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 1038
LENGTH: 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1038, Application US/10472928 Publication No. US20050020813A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
FEATURE:
FEATURE:
OTHER INFORMATION: PTS system, beta-glucosides-specific IIABC components
OTHER INFORMATION: Cellular location: membrane
OTHER INFORMATION: Similar to strain R6 sequence 15902549 (0.E+01)
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/472,928 CURRENT FILING DATE: 2003-09-26
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APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE:
FILE REFERENCE: P026926WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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ATKRFGGNEFLGAGIGMAMVFFTLVNGYDVAATMTAGEMPMWSLFGLDVAQAGYQGTVLF
                                                                                           IPILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFT
                                                                                                                                  YQIILG-NDVANYYKEFVKLGNFESDSV---
                                                                                                                                                                     FQIIVGPGDVDHVFKE---LDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPL
                                                                                                                                                                                                          MSYKDTVQKILDVIGGEKNVNRVTHCVTRLRLELKDENLVNDDDVKKIPGVIGIMKKNGQ
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                                                                                                                                                                                                                                                                                      Conservative
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RESULT 10
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Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-05-26
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               APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                            APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                        FILING DATE:
                                                                                                         APPLICATION NUMBER: 60/257,931
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Prior Application data removed -
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Forsyth, R.
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; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74439
                                                                                                                                                                                                                           RESULT 11
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                                                                                                                                Sequence 70209, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
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SOFTWARE: PATENTIN VERSION:
SEQ ID NO 74439
LENGTH: 620
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Best Local Similarity
                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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                                                            APPLICANT:
                  APPLICANT
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Yamamoto, ku
                                                                                      Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
                                                                                                                                                                                                                                                                                               KKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSN 627
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          Carr, Grant
                                                          Zyskind, Judith Wall, Daniel
                                              Trawick, John
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APPLICANT: Xu, H.

FILE OF INVENTION: Identification of Essential Gen
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/91,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-09-06
PRIOR FILLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 144;
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Best Local Similarity 39.5%;
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353
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                                                                  SIGGTYLWPIVAISNICQGSAAFGAWFVYKRRKMVKEEGLALTSCISGMLGVTEPAMFG
                                  VTFVI 453
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Pred. No. 6.9e-55;
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RESULT 12
US-09-718-626-6961
; Sequence 6961, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:

APPLICANT: NAKAGAWA,

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PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6961
LENGTH: 683
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION:
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Similarity 30.9%;
GHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKA
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                                                   LAAGEVVDIVSPLEGKAIPLSEVPDPIFAAGKLGPGIAIQPTGNTVVAPADATVILVQKS
                                                                                                                    SNEERDEARAKVAADKQAEEDLKAEANATPAAPVAAAGAGAGAGAGAAAGAATAVAAKPK 525
                                                                                                                                                   RNGSID-----PAGTTKAEAEAPA
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TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                EFSNDSTIĮQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPS
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ANDO, SEIKO
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OCHIAI, KEIKO
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Sequence 26, Application US/10450055
Publication No. US20040043953A1
GENERAL INFORMATION:
APPLICANT: BASF Aktiengesellschaft
FITLE OF INVENTION: No. US20040043953A1el genes of Cor
FILE REFERENCE: 936 2000
CURRENT APPLICATION NUMBER: US/10/450,055
CURRENT FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 26
LENGTH: 683
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-450-055-26
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                                                                       LAAGEVVDÍVSPLEGKÁÍPLSEVPDPÍFAAGKLGPGIAÍQPTGNTVVAPADATVILVQKS
                                                                                                       EFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAFPS
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
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Best Local Similarity
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TITLE OF INVENTION: Identification of Essential Genes
FILE REFERENCE: ELITEA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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LOCATION: (223)..(223)
OTHER INFORMATION: X=any amino acid
                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-12-22
121 LVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLFVLVGFTATK
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                                                                                                                                                                    WDHKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM
                                                          FQVIIG-GDVKFVFAEIDKL--GDFSASKESSSE--ANNKGIVSKVLDTIAGIFVPIVPA
                                                                                              FQIIVGPGDVDHVFKELDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPLIPI 120
                                                                                                                                 MGYKELGKDILANVGGSENVSSLAHCATRLR--FKDDSKADESAIRNLKGVVGVVNQGGQ
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Zamudio, cm.
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Zyskind, Judith
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Yamamoto, Robert
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SEQ ID NO 367
LENGTH: 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
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TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AM100649-PCT
     341
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     AAAGLDDTTMVIVTNTGDYASVAPVAT---GSVAKGDAVIEV 379
                                       KAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEAGANLLNV
                                                                                                     PSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEFDIDAI
                                                                                                                                                                        PAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKGQLVSPVSGKIVVAF
                                                                                                                                                                                                                           YVGNGQLPQYLLMVAVSFALGFALTYMFGY-----EDEVDATAAAKRAEVAEEKEEVA
                                                                                                                                                                                                                                                                                                       LGITEPAIFGVNLRFRKPFFLSLIAGAIGGGLASI-----LGLAGTGNGITIIPGTML
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                                                                            PTGHAFGLKTR----NGAEVLIHVGIDTVSMNGDGFETKVAQGNKVKAGDVLGTFDSNKI
                                                                                                                                                    PAALQNETLV--TPIVGDVVALADVNDPVFSSGAMGQGIVVKPSQGVVYAPADAEVSIAF
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Pred. No. 1.3e-41;
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POLYP

Search completed: March 7, 2005, 22:08:07 Job time : 139 secs

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	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - prot	OM protein - protein search, using sw model
Run on:	March 7, 2005, 22:05:18 ; Search time 44 Seconds (without alignments) 1445.438 Million cell updates/sec
Title: Perfect score: 3 Sequence: 3	US-10-019-284B-2 3342 1 MDHKDLAQRILRDIGGEDNIIEAGANLLNVAKKEAVPATP 661
Scoring table: I	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283416 segs, 96216763 residues
Total number of 1	Total number of hits satisfying chosen parameters: 283416
Minimum DB seq lo Maximum DB seq lo	seq length: 0 seq length: 2000000000
Post-processing: Minimum Match Maximum Match Listing first	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	PIR 79:* 1: Dir1:* 2: Dir2:* 3: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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24.4	24.6	24.7	24.8	25.7	<u>ب</u>	26.5	٥.	.7	27.7	27.7	7.	7.	7.	7.	8	8	8	28.7	9	9		32.0	ν.	32.9	'n		44.2	48.2	Match	Query
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phosphotransierase	hypothetical prote	phosphotransferase	phosphotransferase	beta-glucoside-spe	PTS system, beta-g	hypothetical prote	beta-glucoside-spe	ide pe	PTS system, beta-g	beta-	system, beta-		hypothetical prote	phosphotransferase	trehalose PTS syst	phosphotransferase	phosphotransferase	PTS system IIABC c	phosphotransferase	œ	PTS system, trehal	þ	PTS system, sucros	fusion, PTS system	PTS system, sucros	scrA protein - Sta	phosphotransferase	hotransfera	Description	

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472	372	478	473	473	473	483	494	459	494	640	460	455	458	612	612
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AF1058	I39868	B82263	A86122	C65236	A98281	AI0449	AF1585	JU0293	AG1231	AB1423	A39938	WOEBST	H83881	B95067	A97935
protein-Npi-phosph	sac operon regulat	PTS system, trehal	PTS system enzyme	phosphotransferase	trehalose specific	protein-Npi-phosph	PTS system trehalo	levansucrase synth	PTS system trehalo	beta-glucoside-spe	phosphotransferase	phosphotransferase	PTS system, sucros	hypothetical prote	hypothetical prote

ALIGNMENTS

phosphotransferase system enzyme II (EC 2.7.1.69), sucrose specific - Pediococcus pentos (;Species: Pediococcus pentosaceus (;Species: Pediococcus pentosaceus (;Pate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 (;Accession: S44257 R;Leenhouts, K.K.J.; Bolhuis, A.A.; Kok, J.J.; Venema, G.G. submitted to the EMBL Data Library, April 1994 A;Pescription: The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0. A;Reference number: S44252 A;Accession: S44257 A;Gene: scrA C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase C;Keywords: phosphotransferase F;488-640/Domain: phosphotransferase system glucose-specific enzyme II, factor III homol 밁 밁 Ś 밁 Ś 밁 á δ A;Molecule type: DNA A;Residues: 1-651 <LEE> A;Cross-references: UNIPROT:P43470; EMBL:Z32771; NID:g493728; PIDN:CAA83668.1; PID:g475. C;Genetics: 밁 문 S Matches 331; Query Match Best Local Match 48.2%; Score 1609.5; DB 2; Local Similarity 49.6%; Pred. No. 1.9e-99; 355 AACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGALI 414 359 299 179 179 119 119 PILVGGGILMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTA 178 299 239 LGVAFILATLEKFFHKHIKGAFDFTFTPMFAIVITGFLTFTIVGPVLRTVSDALTNGLVG 239 60 YQIIIGPGDVDKVYDALIVKTGLK-EVTPDDIKAVAAAGQNKNPLMDFLKVLSDIFIPIV 61 FQIIVGPGDVDHVFKELDDATSKDIAVSTEQLKDVVA--NNANWFSRAVKVLADIFVPLI 118 LYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQG 354 AATLAIFFATKSQKQKALTSSAGVSALLGITEPAIFGVNLKMKFPFVFAAIASGIASAFL LYNSTGWIGMGIFGLLYSAIVITGLHQTFPAIETQLLANVAKTGGSFIFPVASMANIGQG TKREGGNEFLGAGIGMAMVEPTLVNGYDVAATMTAGEMPMWSLEGLDVAQAGYQGTVLPV MNHQEVADRVLNAI-GKNNIQAAAHCATRLRLVIKDESKIDQQALDDDADVKGTFETNGQ TKRFGGNPYLGATMGMIMVLPSLVNGYSVATTMAAGKMVYWNVFGLHVAQAGYQGQVLPV PALVAGGLLMALNNVLTAEHLFMAKSVVEVYPGLKGIAEMINAMASAPFTFLPILLGFSA Conservative 114; Mismatches 196; Indels Length 651; 27; 418 298 238 59 358 298 238 178 60

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RESULT 2
B32243
phosphotransferase system enzyme II (EC 2.7.1.69), sucrose. C;Species: Streptococcus mutans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_cl C;Accession: B32243
R;Sato, Y; Poy, F; Jacobson, G.R.; Kuramitsu, H.K.
J. Bacteriol. 171, 263-271, 1989
A;Title: Characterization and sequence analysis of the scr A;Reference number: A32243; MUID:89123027; PMID:2536656
A;Accession: B32243
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A;Residues: 1-664 <SAT>
A;Cross-references: UNIPROT:P12655; GB:M22711; NID:g153799; PIDN:AAA26971.1; PID:g153801
A;Cross-references: UNIPROT:P12655; GB:M22711; NID:g153799; PIDN:AAA26971.1; PID:g153801
C;Superfamily: phosphotransferase system enzyme II sucrose-specific; phosphotransferase
C;Keywords: phosphoprotein; phosphotransferase
C;Keywords: phosphoprotein; phosphotransferase
F;511-664/Domain: phosphotransferase system glucose-specific enzyme II, factor III homol
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                                                                                                                   LAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELEL---FNQG---
                                                                                                                                                                TYQVIPVLVAVWLLSILEKFFHKRLPSAVDFTFTPLLSVIITGFLTFIVIGPVMKEVSDW
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TAAIGGALIALFDIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFVIAFGAAIAYGLYL
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Pred. No. 1e-9
7; Mismatches
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C;Species: Staphylococcus xylosus
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
C;Accession: S39978
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Mol. Gen. Genet. 241, 33-41, 1993
A;Title: Cloning and characterization of the scrA gene of the scr
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A;Residues: 1-480 <WAG>
A;Cross-references: UNIPROT:P51184; EMBL:X69800; NID:g407905; PIDN:CAA49461.1;
C;Superfamily: phosphotransferase system sucrose-specific enzyme II, factor II
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                                                                                                                                                                                                                   LVATYILATIEKGLRKVIPTVLDNLLTPLLAILSTGFITFSFVGPLTRTLGYWLSDGLTW
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                                               TALFDIKAVALGAAGFLGVVSIDAPD--MVMFLVCAVVTFVIAFGAAIAYGLYLVRRN
                                                                                                                                               LYEFGGAIGGLIFGLLYAPIVITGMHHSFIAIETQLIADSSSTGGSFIFPIATMSNIAQG
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               IAFFKVKAIALGTAGIPGFISISGQNNGWLHYGIAMIIAFIVAFGVTYALSYRKKYRN
                                                                                                               AACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGAL
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Pred. No. 3.7e-74;
3; Mismatches 133;
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fusion, PTS system, beta-glucosides specific IIABC component C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_cha C;Accession: H96951
R;Nolling, J; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Sol A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: H96951
A;Status: preliminary
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-200
C;Accession: D90038
R;Kuroda, M; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1255-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aur
A;Reference number: A89758; MUID:21311952; PMID:11418146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-480 < KUR>
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Best Local S
Matches 242
                                                                                                                                       Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004; Accession: H96951
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                                                                                                                                                                                                                                                                                                                                                                                                     AACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YQIIIGSGTVNKVFSELEKLTGKE-ASTTSEVKAQSAKNMNPLQRFVKMLSDIFVPIIPA
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6.8e-71;
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Sekimizu,
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K.;
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A;Reference number: A82035; A;Accession: F82432 A;Status: preliminary A;Molecule type: DNA

A;Residues: 1-479 <HEI>

A; Title: DNA Sequence of both chromosomes of the cholera A; Reference number: A82035; MUID: 20406833; PMID: 10952301

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, Nature 406, 477-483, 2000

Fraser, C

; Clayton, F ; Bass, S.; r, C.M.

Qin,

pathogen

Vibrio cholerae

R.A.;

Gwinn, M.L.; H.; Dragoi, 1

Ι.,

Dodson, R.J I.; Sellers,

٠,

C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82432

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A;Molecule type: DNA
A;Residues: 1-627 <KUN>
A;Residues: 1-627 <KUN>
A;Cross-references: UNIPROT:Q9L8G6; GB:AE001437; PIDN:AAK78403.1;
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0423
C;Superfamily: phosphotransferase system enzyme II sucrose-specifi
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sucrose-specific IIBC
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                                                                                                                     GDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNT
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                                                                                     GEEVKKGDKLIQFDLDLVKEKAVSPIVLTIVTNHEDMGFVNS
                                                                                                                                                       PEDGEVVSPIDGTVVHVFETKHAIAMKSK----NGVEMLIHIGIDTVKMEGNGFKSFIND
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                                                                                                                                                                                                                                                                                                                            ALFDIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFVIAFGAAIAYGLYLVRRNGSIDP
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component
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VCA0653 [imported]
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    Vibrio cholerae

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R;Blatch, G.L.; Scholle, R.R.; Woods, D.R.
Gene 95, 17-23, 1990
Gene 95, 17-23, 1990
A;Title: Nucleotide sequence and analysis of the Vibrio alginolyticus
A;Reference number: JQ0781; MUID:91071601; PMID:2174811
A;Accession: JQ0781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sucrose uptake protein - Vibrio alginolyticus
N;Alternate names: enzyme II-sucrose protein
C;Species: Vibrio alginolyticus
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
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A;Map position: 2
C;Superfamily: phosphotransferase
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P22825; GB:M76768; GB:M30194; NID:g155261; PIDN;AAA27555.1; C;Genetics:
                                                                                                                                                                                                                                                                                                             A; Status: preliminary
A; Molecule type: DNA
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  FQIIVGPGDVDHVFKELDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPLIPI 120
                                                                                 MDHKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM
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                                          MNYPAVAKELLTLLGGKSNITALAHCATRLRLAVADEQKIDEQAIDNLEGVKGQFKVAGQ
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                                                                                                                                            32.0%; Score 1069; DB 2; 46.1%; Pred. No. 1.2e-63;
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Pred. No. 3.1e-65;
5; Mismatches 151;
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                                                                                                                              Mismatches 151;
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A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A33650; MUID:20512582; PMID:11058132
A;Accession: H83926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change
C;Accession: H83926
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A; Residues: 1-470 < STO>
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  296 LQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-GGSFIFATASMANIAQG 354
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                                                                                                                                                                                                                                                                                            64 VIIGQGTVDKVYKELVAETGIGEATKEDV------KDAAAKNTNVFQRAVKTLADIFIP 116
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                                                                            LPVLVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDLLAHG 295
                                                                                                                                               FTATKRFGGNEFLGAGIGMAMVFPTLVNGYDVAATMTAGEMPMWSLFGLDVAQAGYQGTV 235
                                                                                                                                                                                                             ILPAIVTAGLLMGINNILTAEGIFYDGASVIDIHPQWADFAGIINLIANTAFVFLPGLIG 176
                                                                                                                                                                                                                                                                                                                            IIVGPGDVDHVFKEL-----DATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVP 116
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                                          LPILFSAWILAKIBIFLRKRVPDSIQLLVVAPVALLITGFIAFAAIGPITFTIGNGITNV 296
                                                                                                                           WSAVKRFGGSELLGIVLGLMLVHPDLLNAWGYGQAQLEGEIPTWNLFGLTIEQVGYQGQV
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phosphotransferase system enzyme II (EC 2.7:1.69) phosphoenolpyruvate-dependent, trehald C;Species: Bacillus subtilis C;Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change O9-Jul-2004 C;Accession: C69725; S67929; JC5037; 140497; S67864
C;Accession: C69725; S67929; JC5037; 140497; S67864
C;Accession: C69725; S67929; JC5037; 140497; S67864
C;Accession: C69725; S67929; JC5037; 140497; S67864
C;Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc R;Kunst, F.; Damearson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Rature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holeappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Fark, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Ogawa, K.; Ogiwara, A.; Oudega, B.; Fark, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A; Hiller, The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Rocles on C69725
A; Status nucleic acid servence of the Gram-positive bacterium Bacillus subtilis.
                                                                                                                                               F;113-131/Domain: transmembrane #s
F;160-181/Domain: transmembrane #s
F;184-203/Domain: transmembrane #s
F;230-245/Domain: transmembrane #s
F;230-245/Domain: transmembrane #s
F;263-286/Domain: transmembrane #s
F;305-325/Domain: transmembrane #s
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C69725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-139,'S',141-362,'L',364-464,'G',466-470 <SC2>
A;Cross-references: EMBL:Z54245; NID:g1000450; PIDN:CAA91014.1; PID:g1000451
C;Comment: This enzyme functions as the specific trehalose transporter. It belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Schoeck, F.; Dahl, M.K.

Gene 175, 59-63, 1996
A;Title: Analysis of DNA flanking the treA gene of Bacillus
A;Reference number: JC5037; MUID:97074649; PMID:8917076
A;Accession: JC5037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: strain 168
R;Helfert, C.; Gotsche, S.; Dahl, M.K.
Mol. Microbiol. 16, 111-120, 1995
A;Title: Cleavage of trehalose-phosphate in Bacillus subtilis is catalysed by A;Reference number: I40497; MUID:95379486; PMID:7651129
A;Accession: S67929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Residues: 1-470 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 324-362,'L',364-464,'G',466-470 <HEL>
A;Cross-references: EMBL:X80203; NID:g580941
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                                                                                                                                                                                                                                                                                                                                                           Superfamily: phosphotransferase system sucrose-specific keywords: phosphotransferase; sugar transport system
Query Match
Best Local Similarity
Matches 203; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGALI 414
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29.9%; Silarity 43.9%; P
Conservative 93;
                                                                                                            p: sugar transport system
the #status predicted <TM1>
the #status predicted <TM2>
the #status predicted <TM3>
the #status predicted <TM4>
the #status predicted <TM5>
the #status predicted <TM5>
the #status predicted <TM6>
the #status predicted <TM7>
the #status predicted <TM7>
the #status predicted <TM7>
the #status predicted <TM8>
Score 999; DB
Pred. No. 5.4e-
93; Mismatches
                         DB 2;
   160;
                                                         Length 470;
   Indels
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 236
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rdos

Local Similarity

Conservative

29.6%; Score 990.5; DB 2; 35.5%; Pred. No. 2.8e-58; ative 114; Mismatches 270;

Length Indels

632; 45;

1 MDHKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM

FQIIVGPGDVDHVFKELDD---ATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPL 117 MDNKQIAKEVIEALGGRDNVRSVAHCATRLRVMVVDEAKIDKERAENIDKVKGAFFNSGQ

118 116

IPILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMIN-----

IPVLVATGLEMGLRGLLTNDTFLG

-FFGASSKDINANFILYTQVLTDTAFAF

166

-LMASAPFAF 169

115

60

60

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Infect. Immun. 61, 2602-2610, 1993
A;Title: Sequence analysis of scrA and scrB from Streptococcus sobrinus 6715.
A;Reference number: S68598; MUID:93273516; PMID:8500898
                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-632 <CHE>
                                                                                                                                               A; Reference number: S68598; A; Accession: S68599
                                                                                                                                                                                                                                         R; Chen, Y.Y.M.;
                                                                                                                                                                                                                                                                  C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997
C;Accession: S68599
                                                                                                                                                                                                                                                                                                               phosphotransferase system enzyme II N;Alternate names: sucrose-specific C;Species: Streptococcus sobrinus A;Variety: strain 6715
A;Gene: scrA
                                             A; Cross-references: EMBL:L06791
                                                                                                                                                                                                                                                                                                                                                                                                                   S68599
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                      ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALGAAGFLGVVSIDAPDMVMFLVCAVVTFVIAFGAAIAYGLY 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGALIALFDIKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ--GGSFIFATASMANIAQGAACLAVFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LATIEKFLHKRLMGTADFLITFVLTLTLLTGFLTFIAIGPAMRWVGDLLAHGLQGLYDFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLMAINNVLVAQDL-FGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTATKRFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGTVNKVYAELVKETG--IGESTKDEVKKASEKNMNPLQRAVKTLADIFIPILPAIVTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVGVGGVPGIFSIMSQYWGAFAIGMAIVLIVPFAGTYAYARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVKDEKQKGLSLTSGISAYLGITEPÄIFGVNLRYRFPFIIAMVSSGLAGMYISSQGVLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAKIEVFLTKRTPEGIQLLVVAPITLLLTGFASFIIIGPITFAIGNVLTSGLISVFGSFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALGGLLYGGFYSALVITGMHTFLAVDLQLIGSKLGGTFLWPMLALSNIAQGSAALAMMF
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                                                                                                                                                                                                                                         Lee, L.N.; LeBlanc, D.J.
                                                                                                                                                                                                                                                                                                                                                                    (EC 2.7.1. enzyme II
                                                                                                                                                                                                                                                                                                                                                                    enzyme
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PTS system IIABC components [imported] - Streptococcus pneumoniae (strain 'C'Species: Streptococcus pneumoniae C'Species: Streptococcus pneumoniae C'Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-200. C'Accession: F95200
C'Accession: F95200
R'Tettelin, H. Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Pete: On, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D. On, J. Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A; Nuthors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A; Nitle: Complete Genome Sequence of a virulent isolate of Streptococcus p. A; Reference number: A95000; MUID:21357209; PMID:11463916
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A; Residues: 1-627 < KUR>
A; Cross-references: UNIDROT: Q97PB8;
A; Experimental source: strain TIGR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Streptococcus pneumoniae;
;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004;Accession: F95200
                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary
                                                                                                                                                                                                                                                                                         Superfamily:
                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGGALIALFDIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFVIAFGAAIAYGLYLVRR
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                                                                                                                                                  MDHKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKEEDVSAKKPEAPAAAPVAETETKSE-----VIASPLDGEAVELSKVNDPVFSSEAMG
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                                                                                                                           MNNQEIAKKVIDALGGRENVNSVAHCATRLRVMVKDEKINKEVIENLEKVQGAFFNSGQ
    IPILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFT
                                                                              FQIIVGPGDVDHVFKE---LDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LELNK
                                                YQIIFGTGTVNKMYDEVVVLGLPTS----SKDDMKAEVAKQGNWFQRAIRTFGDVFVPI
                                                                                                                                                                                                                                                                                       phosphotransferase system enzyme II sucrose-specific;
                                                                                                                                                                                                            Conservative 141; Mismatches 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    632
                                                                                                                                                                                                                         28.7%; Score
33.3%; Pred.
                                                                                                                                                                                                                               Score 960; DB 2;
Pred. No. 3e-56;
                                                                                                                                                                                                                                                                                                                                                                       GB:AE005672; PIDN:AAK75799.1; PID:g14973217; GSPDB
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Radune, D.; Holtzapple,
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|PVIVATGLFMGVRGLFNALEM---
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                                                                                                                                                                                                                                                                                                                                                                              TFRVFGGNPAVGIVLGMMLVSGSLPNAWAVA---QGGEVTAMNFFGF-IPVVGLQGSVLP
                                                                                                                                                             NGSIDPDATAAPVPAGTTKAEAE-APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKL
                                                                                                                                                                                                                                                                                                       GLYDFGGFVGGLLFGLVYSFIVITGLHQSFPFIELELFNQGGSFIF-ATASMANIAQGAA
                                                                                         GSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTH
                                                                                                                                                                                       -----LGLAGTGNGITÍIPGTMLYVGNGQLPQYLLMVAVSFALGFALTYMFGY----
GDAVIEV
                      GANLLNV
                                                                 FNPLKKOGDEVKAGELLCEFDIDALKAAGYEVTTPIVVSN---YKKTGPVNTYGLGEIEA 644
                                                                                                                                        --EDEVDATAAAKRAEVAEEKEEVAPAALQNETLV--TPIVGDVVALADVNDPVFSSGAM
                                                                                                                                                                                                              FDIKAVALGAAGFLGVVSIDAPDMV------MFLVCAVVTFVIAFGAAIAYGLYLVRR
                                             FETKVAQGNKVKAGDVLGTFDSNKIAAAGLDDTTMVIVTNTGDYASVAPVAT---GSVAK 618
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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1167 RESULT 12 AB1167 phosphotransferase system (PTS) beta-glucoside-specific enzyme IIABC component C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1167 A;Status: preliminary A;Molecule type: DNA R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Maitournam, A.; Ma Voss, H.; Wehland, ; Bloecker Fsihi, H. homolog

A;Cross-references: UNIPROT:Q8Y904; A;Experimental source: strain EGD-e A; Residues: 1-617 <GLA> GB:NC_003210; PIDN:CAC98816.1; PID:g16410127; GSPDB

A;Gene: lmo0738 C;Superfamily: phosphotransferase system enzyme II sucrose-specific; Genetics:

Similarity 28.6%; Score 957; DB 2; 1 ilarity 35.1%; Pred. No. 4.6e-56; Conservative 124; Mismatches 228; Length

phosphotransferase

片 Ś Query Match Best Local S Matches 225 225; MDHXDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM FQIIVG--PGDVDHV---FKELDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFV 115 MDYOKLAKEILANVGGEENVRSVVHCATRLRFKLVNKEKADKKOIESISGVISVVENAGO Indels Gaps 60 60 17

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A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A, Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Recession: B98067
                                                                                                                                                                                                        A;Status: P---- DNA
A;Molecule type: DNA
A;Residues: 1-627 <KUR>
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                                            MNNQEIAKKVIDALGGRENVNSVAHCATRLRVMVKDEEKINKEVIENLEKVQGAFFNSGQ
                                                           MDHKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQVIIGNTVGDVYKALGSFTKLTDDGDSEIAKGT---KD---SDGNFLSKAIDVISGIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGKGVAIVPQEGKLISPVNGTIETAFPTGHAIGIRS----DKGVEILLHVGFDTVQLNGK 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGT
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                                                                                                     Conservative
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                                                                                                                   28.6%;
33.3%;
                                                                                                    141;
                                                                                                                 Score
Pred.
                                                                                                                                                                                                                      GB:AE007317;
                                                                                                     Mismatches
                                                                                                    e 956; DB 2; L
. No. 5.5e-56;
lsmatches 246;
                                                                                                                                                                          enzyme
                                                                                                                                                                         II sucrose-specific;
                                                                                                                                                                                                                    PIDN: AAL00370.1;
                                                                                                                               Length
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J.; Matsushima, P.; McAhren,
                                                                                                    Indels
                                                                                                                                                                                                                   PID:g15459232;
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GDAVIEV 625
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                                                                                                                                                                                                                                                   NGSIDPDATAAPVPAGTTKAEAE-APAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKL
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                                                                     FEAKVAQGNKVKAGDVLGTFDSNKIAAAGLDDTTMVIVTNTADYASVAPVAT---GSVSK
                                                                                                                                           GQGIAVKPSQGVVYALADAEVSIAFPTGHAFGLKTR----NGAEVLIHVGIDTVSMNGDG
                                                                                                                                                                                                                                                                                                                         FDIKAVALGAAGFLGVVSIDAPDMV-----MFLVCAVVTFVIAFGAAIAYGLYLVRR
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                                                                                                                                                                                                                                                                                         -LGLAGTGNGITIIPGTMLYVGNGQLPQYLLMVAVSFALGFALTYMFGY-----
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RESULT C95220

(strain TIG Heid

HBOH, 1,, 5001
Science 293, 498-506, 2001
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A;Authors: Complete Genome Sequence of a virulent isolate of Streptococcus A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus A;Title: Complete A95000; MUID:21357209; PMID:11463916 T.D.; Peterson, S.; H Radune, D.; Holtzappl B.A.; Morri pneumoniae. Morrison

A;Reference number: A95000; MUID:2135:
A;Accession: C95220
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-655 < KUR>
A;Cross-references: UNIPROT:Q97NW9; GI
A;Experimental source: strain TIGR4 GB:AE005672; PIDN: AAK75956.1; PID:g14973388;

GSPDB:C

A;Gene: SP1884 C;Superfamily: ;Genetics:

phosphotransferase system enzyme II sucrose-specific; Length 655 phosphotransferase

밁 S Local Similarity 34.9 AQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGMFQIIVG AKDLLQAIGGKENVTAVTHCATRMRFVLGDDKKANVKAIESIPAVKGTFTNAGQFQVIIG 28.4%; Score 949; DB 2; 34.9%; Pred. No. 1.7e-55; tive 128; Mismatches 253; 56; Gaps 67

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Query Match
Best Local S
Matches 230
 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFNVTAASIGIGGLPGILSIQPQYMLPFAGTMLVAIVVPMLLTF--
 Conservative
            27.9%;
 130;
Score 934; DB 2;
Pred. No. 1.9e-54;
30; Mismatches 253
                         Length 705
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                                                                                                            NLNGTHFNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKK-----TGPVNT
                                                                                                                                                                                                                                                                                                                                                                                     VPÄYYPMHRHDEREAQVSLPATISÄYLGVTEPÄLFGVNVKYIYPPVAGMTGSÄLAGMLSV
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                                                                           GLDGKGFESLVVQGDHVTVGQQLIRFDMDVIKAAGLVTETPVIITNQDAYTATITGTYPT
                                                                                                                                                      FASGYMGQGLVIEPSQGELTSPVNGTYTVLFPTKHAIGI--VSDEG--VELLIHIGMDTV
                                                                                                                                                                                           FASGKLGSGVAIVFTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTV
                                                                                                                                                                                                                              FTK-----TEGDTNLQAEFVAQEEAEFVSHELVELTSVEIISPLTGQVKELSQATDPV
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Search completed: March Job time : 46 secs 7, 2005, 22:16:51

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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     Score
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933	933.5	933.5	934	934	935.5	937.5	946	949	951.5	954.5	956	956.5	956.5
27.9	27.9	27.9	27.9	27.9	28.0	28.1	28.3	28.4	28.5	28.6	28.6	28.6	28.6
674	475	475	705	619	620	627	614	655	627	475	627	480	475
2	N	N	N	N	N	N	N	2	N	N	N	N	N
Q8K5K9	Q7A7D1	Q99WC9	Q8DNI6	Q65D51	Q99Y91	Q8K5Z4	Q65D36	Q97NW9	Q8NZJ7	Q81HZ5	Q8DNS8	Q9F8X3	Q63G14
Q8k5k9	Q7a7d1	Q99wc9	Q8dni6	Q65d51	Q99y91	Q8k5z4	Q65d36	Q97nw9	Q8nzj7	Q81hz5	Q8dns8	Q9f8x3	Q63g14
9 streptococc	_	•			1 streptococo	4 streptococc	٠,	9 streptococo	7 streptococ	5 bacillus c	~	3 pseudomonas	4 bacillus ce

ALIGNMENTS

		R R A A R A R A R A R A R A A A A A A A		NW DS
erpro; IPRO11 erpro; IPRO01 erpro; IPRO03 erpro; IPRO01 erpro; IPRO10 erpro; IPRO10 erpro; IPRO10 erpro; IPRO10 em; PPO0358; Em; PPO0378; Em; PPO0378; Em; PPO01476 Dom; PDO01476	vitamins."; sjotechnol. 104:5-25(2003). L; AP005282; BAC00036.1; L; BX927155; CAF21304.1; C; BX927155; Creembrane; IEA. GO:0016020; C:membrane; IEA. GO:0008982; F:protein-N(PI)-phos GO:0005351; F:sugar porter activ GO:0005401; P:prosphoenolpyruvat GO:0006810; P:transport; IEA.	[2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025; STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025; STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025; STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025; STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025; STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025; STRAIN-ATCC 13032 / DSM 1	Name=ptsS; OrderedLocusNames=Cg12642, cg2925; Name=ptsS; OrderedLocusNames=Cg12642, cg2925; Corynebacterium glutamicum (Brevibacterium flavum). Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium. NCBI_TaxID=1718; [1] SEQUENCE FROM N.A. STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025 Nakagawa; Nakagawa S.; Wakagawa S.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.	D6 D8NMD6 PRELIMINARY; PRT; 661 AA. Q8NMD6; Q6M2U8; O1-OCT-2002 (TrEMBLrel. 22, Created) O1-OCT-2002 (TrEMBLrel. 22, Last sequence update) O2-OCT-2004 (TrEMBLrel. 22, Last sequence update) Phosphotransferase system IIC components, glucose/maltose/N- acetylglucosamine-specific (EC 2.7.1.69) (ENZYME II SUCROSE

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RESULT 2
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ID PTSA PEDPE
AC P43470;
DT 01-NOV-1995 (
DT 05-JUL-2004 (
DT PS System, s
DE PTS System, s
DE permease IIAB
DE component) (E
GN Name=scra,
OX NCBI_TaxID=12
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TIGRPAMS; TIGR01996; PTS-II-BC-Sucr;
PROSITE; PS01035; PTS_EIIB_CYS; 1.
Complete proteome; Transferase.
SEQUENCE 661 AA; 69148 MW; COE5E:
                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
PTS system, sucrose-specific IIABC component
permease IIABC component) (Phosphotransferase
component) (EC 2.7.1.69) (EII-Scr).
               Pediococcus pentosaceus
Bacteria; Firmicutes; La
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  _TaxID=1255;
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Pred. No. 3.3e
4; Mismatches
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3.3e-191;
ches 3;
                 Lactobacillaceae;
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                                                                  (EIIABC-
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                                                                  -Scr)
                  Pediococcus
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Matches 331
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ProDom; PD0012243; PTS EIIA; 1.
TIGRFAMS; TIGR00826; EIIB glc; 1.
TIGRFAMS; TIGR00830; PTBA; 1.
TIGRFAMS; TIGR01995; PTS-II-ABC-beta; 1
TIGRFAMS; TIGR01996; PTS-II-BC-sucr; 1.
TIGRFAMS; TIGR01992; PTS-IIBC-Tre; 1.
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SEQUENCE FROM N.A.
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Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF02378; PTS_EIIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z32771; CAA83668.1;
EMBL; L32093; AAA25567.1;
PIR; S44257; S44257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (Stor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR011055; Dup_hybrid_motif.
InterPro; IPR001996; Ptrans_BIIB.
InterPro; IPR003152; Ptrans_BIIC.
InterPro; IPR001127; PTS_BIIA.
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                                                                                                                                                                                                                                                                                                                                Phosphorylation; Phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation.

European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no we by non-profit institutions as long as its content is in no we life of the statement is not removed. Usage by and for commercial field and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the sugar.
CATALYTIC ACTIVITY: Protein N-phosphohistidine +
histidine + sugar phosphate.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Contains 1 PTS EIIA domain.
SIMILARITY: Contains 1 PTS EIIB domain.
SIMILARITY: Contains 1 PTS EIIC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: This is a component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active transport system. The IICD domains contain the sugar binding site and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPT); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to
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; P20166; 1GPR.
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                                                FQIIVGPGDVDHVFKELDDATSKDIAVSTBQLKDVVA--NNANWFSRAVKVLADIFVPLI 118
                                                                                       MNHQEVADRVLNAI-GKNNIQAAAHCATRLRLVIKDESKIDQQALDDDADVKGTFETNGQ
                                                                                                     MDHKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM
PILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTA
                             YQIIIGPGDVDKVYDALIVKTGLK-EVTPDDIKAVAAAGQNKNPLMDFLKVLSDIFIPIV
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nilarity 49.6%;
Conservative 114
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EIIC.
EIIA.
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Phosphohistidine (By
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Phosphohistidine (Bo
Phosphohistidine (Bo
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Phosphohistidine (Bo
                                                                                                                                                  Score 1609.5; DB
Pred. No. 8.8e-89;
4; Mismatches 196
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RESTRAIN=NCIMB 8826 / WCFS1;

RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;

RX Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,

RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,

RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,

RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing I

RA De Vos W.M., Siezen R.J.;

RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";

RT Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).

DR EMBL; ALD95252; Cande3855.1; -

DR GO; GO:0016020; C:membrane; IEA.

GO; GO:0008982; F:protein.N(PI) phosphohistidine-sugar phosph. .

GO; GO:0008982; F:sugar porter activity; IEA.

GO; GO:00040740; F:transferase activity; IEA.

GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. .

DR GO; GO:0006810; P:transport; IEA.

TnterPro; IPR011055; Dup_hybrid_motif.
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01-JUN-2003 (TremBLrel. 26,
01-MAR-2004 (TremBLrel. 26,
Sucrose PTS, BIIBCA (EC 2.7,
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Bacteria; Firmicutes; La
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Best Local S
Matches 332
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InterPro; IPR00352; Ptrans_EIIC.
InterPro; IPR00352; Ptrans_EIIC.
InterPro; IPR01127; PTS_EIIA,
InterPro; IPR010973; PTS_II BC_sucr.
Pfam; PF00358; PTS_EIIA; 1.
Pfam; PF00367; PTS_EIIG; 1.
Pfonom; PD001476; Ptrans_EIIB; 1.
ProDom; PD0012476; Ptrans_EIIB; 1.
ProDom; PD0012476; PTS_EIIA; 1.
TIGRPAMS; TIGR01996; PTS_II-BC-sucr; 1.
PROSITE; PS010371; PTS_EIIA; 1; 1.
PROSITE; PS01037; PTS_EIIB_CYS; 1.
Complete proteome; Transferase.
SEQUENCE 651 AA; 66514 MW; CBFB5351
                                     Q9S6S6;
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                                                                                                                                                                                                                                                          NPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANL
                                                                                                                                                                                                                                                                                                                             SGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTHF
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                                                                                                                                                     VALTEPTASSVAAT
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                                                                                                                                                                                                                            TTNVQKGDTVHQGDLLGTFDVAALKAANYDPTVMLVVTNTANYANVERLKVTNVQAGEQL
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                                                         PRELIMINARY;
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Pred. No. 1.2e
14; Mismatches
                                                         PRT;
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Best Local S
Matches 313
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InterPro; IPR011956; Ptrans_EIIB.
InterPro; IPR001956; Ptrans_EIIC.
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR010973; PTS_EIIB.
InterPro; IPR010973; PTS_EIIB.
Pfam; PP00356; PTS_EIIB; 1.
Pfam; PP00356; PTS_EIIB; 1.
Pfam; PP00376; PTS_EIIB; 1.
ProDom; PD001476; Ptrans_EIIB; 1.
ProDom; PD001476; Ptrans_EIIB; 1.
ProDom; PD001476; Ptrans_EIIB; 1.
ProDom; PD001476; Ptrans_EIIB; 1.
ProDom; PD001476; Ptrans_EIIA; 1.
TIGRFAMS; TIGR01996; PTS_EIIB_Cys; 1.
PR0SITE; PS001035; PTS_EIIB_CYS; 1.
PR0SITE; PS01035; PTS_EIIB_CYS; 1.
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EMBL; Z97015;
HSSP; P45618;
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Luesink E.J., Marugg J.D., Kuipers O.P., De Vos W.M.;
"Characterization of the divergent sacBK and sacAR operons,
in sucrose utilization by Lactococcus lactis.";
J. Bacteriol. 181:1924-1926(1999).
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01-MAY-2000 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Enzyme II sucrose protein (EC 2.7.1.69).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0016020; C:membrane; IEA.
GO:0008982; F:protein-N(PI)-phosphohistidine-sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0006810; P:transport; IEA.
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LIALFDIKAVALGAAGFLGVVSIDAPDMVMFLVCAVVTFVIAFGAAIAYGLYLVRRNGSI
                                                 QAGATFAILFVTKNIKTKALAAPAGVSAILGITEPALFGINLKLKYPFFIALGASAIGSL
                                                                               QGAACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGA
                                                                                                                                                                                                LYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELFNQ-----
                                                                                                                                                                                                                                                                                                              LVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDLLAHGLQG
                                                                                                                                                                                                                                                                                                                                                                                                                       TKRFGGNEFLGAGIGMAMVFPTLVNGYDVAATMTAGEMPMWSLFGLDVAQAGYQGTVLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MNHKQVAERILNAV-GRDNIQGARHCATRLRLVLKDTGVIDQEALDNDPDLKGTFEAAGQ
                                                                                                                                                          LYNTLGALGMLVFGGFYSAIVVTGLHQSFPAIETMLITNYQHSGIGGDFIFPVAACANMA
                                                                                                                                                                                                                                                                TKRFGGNPYLGAVVGMIMVMPGLINGYNVAEAISNHTMTYWDIFGFKVAQAGYQGQVLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALVAGGLLMALNNALTAEHLFATKSLVEMFPMWKGFADIVNTMSAAPFTFMPILIGYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YQIIVGPGDVNTVYEEFIKLTGISEA-STADLKEIAGSQKKQNPVMALVKLLSDIFVPLI
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                                                                                                                                                                                                                                                                                                                     MEDLINE-22295063; PubMed-12397186; DOI=10.1073/pnas.172501299; Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J., Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P., Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A., Perretti J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sato Y., Poy F., Jacobson G.R., Kuramitsu "Characterization and sequence analysis cenzyme IIScr of the Streptococcus mutans sucrose phosphotransferase system."; J. Bacteriol. 171:263-271(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-OCT-1989 (Rel. 12, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
PTS system, sucrose-specific IIABC component (EIIABC-permease IIABC component) (Phosphotransferase enzyme component) (EC 2-7.1.69) (EII-SCr),
Name=scrA; OrderedLocuéNames=SMU.1841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=GS-5;
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P12655;
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                                                                                                      Sato Y., Yamamoto Y., Kizaki H., Kuramitsu H.K.;
"Isolation, characterization and sequence analysis of the scrK gene
encoding fructokinase of Streptococcus mutans.";
J. Gen. Microbiol. 139:921-927(1993).
-!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent
sugar phosphotransferase system (PTS), a major carbohydrate active
-transport system. The IICD domains contain the sugar binding site
                                                                                                                                                                                                     Sato Y.,
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   the sugar.
- CATALYTIC ACTIVITY: P
- CATALYTIC ACTIVITY: P
                                                         and the transmembrane channel; the IIA domain contains phosphorylation site (the donor is phospho-HPr); IIA transphosphoryl group to the IIB domain which finally transf
 histidine +
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                            Protein N-phosphohistidine +
 Integral membrane
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analysis of the scrA gene encoding
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InterPro; IPRO01996; Ptrans_EIIB.
InterPro; IPRO01996; Ptrans_EIIC.
InterPro; IPRO01127; PTS_EIIA.
InterPro; IPR001127; PTS_EIIA.
InterPro; IPR010973; PTS_II_BC_sucr.
Pfam; PF00358; PTS_EIIB; 1.
Pfam; PF00378; PTS_EIIB; 1.
Pfam; PF00378; PTS_EIIC; 1.
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PROSITE; PS01035; PTS_EIIB_CYS; 1.
Complete proteome; Phosphorylation; Phosphotransferase Sugar transport; Transferase; Transmembrane.

DOMAIN 1 40 EIIB.
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ProDom; PD002243; PTS EIIA; 1.
TIGRPAMS; TIGR00826; EIIB 91c; 1.
TIGRPAMS; TIGR00830; PTBA; 1.
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TIGRPAMS; TIGR01992; PTS-IIBC-Tre; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE015011; AAN59464.1; -. EMBL; D13175; BAA02466.1; -. EMBL; B32243; B32243.
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GO; GO:0008982; F:protein-N(PI)-phosphohistidine-sugar pho
GO; GO:0008382; F:sugar porter activity; IEA.
GO; GO:0005351; F:sugar porter activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008101; P:transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR001055; Dup hybrid motif.
InterPro; IPR001105; PUP NJB-IIB.
InterPro; IPR001127; PTG_EITA.
InterPro; IPR001127; PTG_EITA.
InterPro; IPR001127; PTG_EITA.
InterPro; IPR001127; PTG_EITA.
InterPro; IPR00158; PTG_EITA.
InterPro; IPR00167; PTS_EITA; I.
ProDom; PD00368; PTS_EITA; I.
ProDom; PD002243; PTS_EITA; I.
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01-OCT-2003
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                                                                         TIGRRAMS; TIGRO0830; PTBA; 1.
TIGRFAMS; TIGRO1996; PTS-II-BC-sucr;
PROSITE; PS00371, PTS EIIA 1; 1.
PROSITE; PS01035; PTS_EIIB_CYS; 1.
                                                                                                                                                                                                                                                                                                                   PubMed=12847288; DOI=10.1073/pnas.1332765100; Barrangou R., Altermann E., Hutkins R., Cano R., Kl "Functional and comparative genomic analyses of an fructooligosaccharide utilization by Lactobacillus Proc. Natl. Acad. Sci. U.S.A. 100:8957-8962(2003). EMBL; AY177419; AAO38866.1; -.
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Bacteria; Firmicutes; Lactobacillales;
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                                                                                                                                                                                                                                                                                                          P20166; 1AX3.
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Score 1457; DE
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22; Mismatches
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Q74HI8;
Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A. "The genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533."; Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004). EMBL, AE017206; AAS09702.1; -. EMBL, AE017206; AAS09702.1; -. HSSP; P20166; 1AX3.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008982; F:protein-N(PI)-phosphohistidine-sugar phosph. . GO; GO:0005351; F:sugar porter activity; IEA.
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05-JUL-2004 (TYEMBLYel. 27, Lt
05-JUL-2004 (TYEMBLYel. 27, Lt
05-JUL-2004 (TYEMBLYel. 27, Lt
Phosphoenolpyruvate-dependent
                                                                                                                                                                                                                                                                                                                                             sucrose specific.
OrderedLocusNames=LJ0519;
Lactobacillus johnsonii.
                                                                                                                                                                                                                                                                                  Lactobacillus.
NCBI_TaxID=33959;
                                                                                                                                                                                                               STRAIN=NCC 533;
PubMed=14966310;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes;
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nt sugar phosphotransferase
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Best Local Similarity 45.0%;
Matches 300; Conservative 12
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ProDom; PD001243; PTS EIIA; 1.
TIGRAMS; TIGR00826; BIIB; 1.
TIGRAMS; TIGR00830; PTBA; 1.
TIGRAMS; TIGR01996; PTS-II-BC-sucr; 1.
PROSITE; PS00371; PTS EIIA 1; 1.
PROSITE; PS01035; PTS-EIIB_CYS; 1.
Complete protecome; Pyruvate; Transferase.
SEQUENCE 647 AA; 69202 MW; 95FA74C533CE9541
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Pfam; PF00356; PTS_EIIA_1; 1.
Pfam; PF00367; PTS_EIIB; 1.
Pfam; PF00378; PTS_EIIC; 1.
ProDom; PD001476; Ptrans_EIIB; 1.
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InterPro; IPR011335; EIIB glc:
InterPro; IPR001396; Ptrans_EIIB.
InterPro; IPR001392; Ptrans_EIIC.
InterPro; IPR001127; PTS_EIIA.
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GO; GO:0006810; P:transport; IEA.
InterPro; IPR011055; Dup_hybrid_motif.
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                              |: | |:
LIAVTKR
                                                                                                                                                                                GSGVAIVPTKGQLVSPVSGKIVVAFPSGHAFAVRTKAEDGSNVDILMHIGFDTVNLNGTH
                                                                                                                                                                                                                                                                                                                               LVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDLLAHGLQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKRFGGNEFIGAGIGMAMVFPTLVNGYDVAATMTAGEMPMWSLFGLDVAQAGYQGTVLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PALVAGGLLMALNNFLTSPGLFGAKSVVQMAPNVKGLSEIIQVMSAAPFIFMPILVGMSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQIIVGFGDVDHVFKELDDATSKDIAVSTEQLKDVVANNA--NWFSRAVKVLADIFVFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDHKKVAEAVIEAV-GRDNLVAAAHCATRLRLVLKDDSKVNMKMLDSDPDIKGTFKTNGQ
                                                                                                                                                                                                                                                                               RNGSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKL
                                                                                                                                                                                                                                                                                                                                                                                                         QGAATFAIYFLTKNEKVKGLASSSGVSALLGITEPALFGVNLKYKFFFFCALIGAGVGAA
                                                                                                                                                                                                                                                                                                                                                                                                                            QGAACLAVFFLAKSEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYDFGGFVGGLLFGLVYSFIVITGLHQSFPPIELELFNQ------GGSFIFATASMANIA
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                                                                                                                                     FNPLKKQGDEVKAGELLCEFDIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGAN
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                                                                 LLNVAKK
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%; Pred. No. 5.8e-79
125; Mismatches 20
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RI Science 299:2071-2074(2003).

BR MBL; AE016833; AAO83060.1; -.

BR MBL; AE016833; AAO83060.1; -.

RTIGR; EPA0067; -.

RTIGR; EPA0067; -.

RGO; GO:0016020; C:membrane; IEA.

RGO; GO:0008982; F:protein.N(PI)-phosphohistidine-sugar phosph. ..

RGO; GO:0008982; F:sugar porter activity; IEA.

RGO; GO:0008981; F:sugar porter activity; IEA.

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

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RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

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RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

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RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. ..

RGO; GO:0009401; P:phosphoenolpyruvate-depende
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Matches 286
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Q82YR5;
Q1-JUN-2003
Q1-JUN-2003
Q1-MAR-2004
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Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=V583 / ATCC 700802;

MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;

Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,

Paulsen I.T., Bouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,

Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,

Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty

Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=V583 / ATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTS system, IIABC components
OrderedLocusNames=EFA0067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pTEF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                        PILVGGGLLMAINNVLVAQDLFGPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTA
                                                                                                                                                                                                                                                                                               MDYAKLASDIILAV-GKDNLIAAAHCATRLRLVLKDNTKVNQKALDENPNVKGTFKIDGQ
                                                                                                                                                                                                         YQVIIGAGDVNFVYDELIKKTGLS-ELSTDDLKQIVDKNKKFNPIMALIKLLSEIFVPII
                                                                                                                                                                                                                                             FQIIVGPGDVDHVFKELDDATSKDIAVSTEQLKDVVANNA--NWFSRAVKVLADIFVPLI
                                                                                                                                                                                                                                                                                                                                             MDHKDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM
                       AKREGANQELGAAIGMIMTTPDL
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Streptococcus faecalis).
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24, Last sequence update)
26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             124;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 1345.5;
Pred. No. 6.9e
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                                                                                                              EEMYPAIKGISSMIQLMSAAPFMFLPILVGISA
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                     GGATEYWNI FGYHVAQTNYAYQVI PV
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REMEL, AF401046; AAKS25281; ...

RHSSP; P45618; 2GPR.

RGO; GO:0016020; C:membrane; IEA.

RGO; GO:0008982; F:protein-N(P)-phosphohistidine-sugar phosph.

RGO; GO:0008982; F:protein-N(P)-phosphohistidine-sugar phospho.

RGO; GO:0009401; P:sugar porter activity; IEA.

RGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho.

RGO; GO:0000810]: P:transport; IEA.

RINEETPO; IPRO11055; Dup hybrid motif.

RINEETPO; IPRO11055; Dup hybrid motif.

RINEETPO; IPRO01127; PTS EITA.

RINEETPO; IPRO01127; PTS EITA.

RINEETPO; IPRO01127; PTS EITA.

RFAm; PF00358; PTS EITA. 1.

DR Pfam; PF02378; PTS EITA. 1.

DR Pfam; PF02378; PTS EITA. 1.

DR PFOSITE; PS00371; PTS EITA. 1.

DR PROSITE; PS00371; PTS EITA. 1; 1.
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01-DEC-2001
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dudez A.M., Chaillou S., Hissler L., Stentz R., Champomier-Verges M.C., Alpert C.A., Zagorec M.; "Physical and genetic map of the Lactobacillus samicrobiology 148:421-431(2002).
                                                                                                                                                                                                                                                                                                                                                                                             Dudez A.-M., Chaillo Submitted (JUL-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=21822499; PubMed=11832506;
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                      SEQUENCE FROM N.A.

STRAIN-DSM 20267 / Isolate C2A;

STRAIN-BM 20267 / Isolate C2A;

MEDLINE-94049686; PubMed-8232209;

Wagner E., Goetz F., Brueckner R.;

"Cloning and characterization of the scrA gene
specific Enzyme II of the phosphotransferase sy

Staphylococcus xylosus.";

Mol. Gen. Genet. 241:33-41(1993).

-!- FUNCTION: This is a component of the phosph
                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
PTS system, sucrose-specific IIBC component (
permease IIBC component) (Phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                  permease IIBC component) (EC 2.7.1.69) (EII-Scr).
                                                                                                                                                                          Staphylococcus xylosus.
Bacteria; Firmicutes; E
                                                                                                                                                         NCBI_TaxID=1288;
                                                                                                                                                                                                      Name=scrA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Loca.
FUNCTION: This is a component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active -transport system. The IICD domains contain the sugar binding site
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InterPro; IPR001996; Ptrans EIIB.
InterPro; IPR003352; Ptrans EIIC.
InterPro; IPR019973; PTS II BC sucr.
Pfam; PF00367; PTS EIIB; 1.
Pfam; PF02378; PTS EIIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD001476; Ptrans EIIB; 1.
TIGRPAMS; TIGR00826; EIIB glc; 1.
TIGREAMS; TIGR00995; PTS-II-ABC-beta; 1.
TIGREAMS; TIGR01996; PTS-II-BC-bucr; 1.
TIGREAMS; TIGR01996; PTS-IIBC-Tre; 1.
PROSITE; PS010035; PTS-EIIB CVS; 1.
Inner membrane; Phosphorylation; Phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X69800; CAA49461.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the sugar.

CATALTYIC ACTIVITY: Protein N-phosphohistidine histidine + sugar phosphate.

SUBCELLULAR LOCATION: Integral membrane protein SIMILARITY: Contains 1 PTS EIIB domain.

SIMILARITY: Contains 1 PTS EIIC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and the transmembrane channel; the IIA domain contains the primary phosphorylation site (the donor is phospho-HPr); IIA transfers its phosphoryl group to the IIB domain which finally transfers it to the sugar.
                                                                    355
               414
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                      LVGGGLLMAINNVLVAQDLF-GPQSLVEMFPQISGVAEMINLMASAPFAFLPVLVGFTAT
                                                                                                                                                                                                                                                                                                               FQIIVGPGDVDHVFKELDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPLIFI 120
 IALFDIKAVALGAAGFLGVVSIDAPD--MVMFLVCAVVTFVIAFGAAIAYGLYLVRRN
                                          AACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWFFYIGIGTAAIGGAL
                                                                                                             Lydfggfvggllfglvyspivitglhosfppielelf----noggsfifatasmaniaog
                                                                                                                                                     LVATYILATIEKGLRKVIPTVLDNLLTPLLAILSTGFITFSFVGPLTRTLGYWLSDGLTW
                                                                                                                                                                        LVVSWILATIEKFLHKRLMGTADFLITFVLTLLLTGFLTFIAIGPAMRWVGDLLAHGLQG
                                                                                                                                                                                                        KRFGGNAYLGAALGMILVHPELMSAYDYPKALEAGKEIPHWNLFGLEINQVGYQGQVLPM
                                                                                                                                                                                                                         KREGGNEFLGAGIGWAMVEPTLVNGYDVAAIMTAG-EMPMWSLEGLDVAQAGYQGTVLPV
                                                                                                                                                                                                                                                              IVAGGLLMGINNILTAPGIFYDNOSLIEVONOFSGLAEMINIFANAPFTLLPILIGFSAA
                                                                                                                                                                                                                                                                                                                                                                       MNYKKSAENILQALGGEDNVEAMTHCATRLRLVLKDEGLVDEKALGDMDVVKGTFSTGGQ
                                                                                                LYEFGGAIGGLIFGLLYAPIVITGMHHSFIAIETQLIADSSSTGGSFIFPIATMSNIAQG
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325
480
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325 P
51326 MW;
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Pred. No. 7e-66;
3; Mismatches 1
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EXIC.
Phosphocysteine (By similarity).
Phosphobistidine (By similarity)
Phosphobistidine (CBy Similarity)
AB4EID9785D84E47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane
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Gaps

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IAFFKVKAIALGTAGIPGFISISGQNNGWLHYGIAMIIAFIVAFGVTYALSYRKKYRN 477

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A Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
A Qin Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
A "Genome-based analysis of virulence genes in a non-biofilm-forming
T "Genome-based analysis of virulence genes in a non-biofilm-forming
T Staphylococcus epidermidis strain (ATCC 12228).";
L Mol. Microbiol. 49:1577-1593 (2003).
EMBL; AED16750; AA005600.1; -.
REMBL; AED16750; AA005600.1; -.
REMBL; AED16750; AA005600.1; -.
RR GO; GO:000593; IIBA.
RGO; GO:000593; F:spacetn-N(Fl).-phosphohistidine-sugar phosph. ..; IE.
GO; GO:000593; F:spacetn-N(Fl).-phosphohistidine-sugar phospho. ..; IE.
RGO; GO:000593; F:spacetn-N(Fl).-phosphoenolpyruvate-dependent sugar phospho. ..; IE.
RGO; GO:0005810; P:transport; IEA.
RGO; GO:0006810; P:transport; IEA.
RGO; GO:006810; P:transport; IEA.
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J-MAR-2004 (TremBirel. 26, La.

E PTS system sucrose-specific IIE
OrderedLocusNames=SE1959;
Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillan-
NCBI_TaxID=1282;
[1]
[1]
SEOTT
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Best Local Similarity
Matches 235; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR011535; EIIB glo.
InterPro; IPR001996; Ptrans EIIB.
InterPro; IPR003352; Ptrans EIIC.
InterPro; IPR003352; Ptrans EIIC.
InterPro; IPR010973; PTS II BC sucr.
Pfam; PF00367; PTS EIIB; 1.
Pfam; PF00378; PTS EIIC; 1.
ProDom; PF001476; Ptrans EIIB; 1.
TIGRPAMS; TIGR01996; PTS-II-BC-sucr; 1.
PROSITE; PS01035; PTS EIIB_CYS; 1.
Complete protons
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Complete proteome.
SEQUENCE 481 AA;
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01-MAR-2003
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                                LYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIELELF----NQGGSFIFATASMANIAQG
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                                                                                                                                      LVVSWILATIEKFLHKRLMGTADFLITPVLTLLLTGFLTFIAIGPAMRWVGDLLAHGLQG
                                                                                                                                                                                                                                           MSYKKSAEETLKAIGGEENLDAMAHCATRLRLVLNDESKVDEDTLSNMDVVKGTFSTGGQ
                                                                                                                                                                                                               KRFGGNPYLGAALGMILVHPGLMSAYDFPKALEEGKAIPHWDVFGLHINEVGYQGQVLPM
LYBFGGAIGGLIFGLLYAPIVITGMHSFIAVETTLIADATKTGGSFIFPIATMSNIAQG
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                                                                                                       EKWLRKVIPTVLDNLLTPLLSIFITAFITFLFVGPVTRQLGYWLSDGLTW
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Last annotation 
IIBC component.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1186; DB 2;
Pred. No. 2.1e-63;
5; Mismatches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local S
Matches 242
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R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0008982; F:protein-N(FI)-phosphohistidine-sugar phose

R GO; GO:0008981; F:sugar porter activity; IEA.

R GO; GO:0005351; F:sugar porter activity; IEA.

R GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phose

R GO; GO:0006810; P:transport; IEA.

R InterPro; IPR011535; BIIB glc.

R InterPro; IPR011535; BIIB glc.

R InterPro; IPR001996; Ptrans_EIIB.

R InterPro; IPR001996; Ptrans_EIIC.

R InterPro; IPR001973; PTS_II BC_sucr.

Pfam; PF00367; PTS_EIIB; 1.

R Pfam; PF00378; PTS_EIIB; 1.

R Pfam; PF00378; PTS_EIIB; 1.

R ProDom; PD001476; Ptrans_EIIB; 1.

R PTGRPAMs; TIGR00826; EIIB glc; 1.

R TIGRPAMs; TIGR00826; PTS_II-BC_sucr; 1.
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Q8NV35;
01-OCT-2002
01-OCT-2002
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PTS system sucrose-specific IIBC component.
Name=scrA; OrderedLocusNames=MW2299;
Staphylococcus aureus (strain MW2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baba T., Takeuchi
Nagai Y., Iwama N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=196620;
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                                                                                                                                                                                                                                                                                                                              FQIIVGPGDVDHVFKELDDATSKDIAVSTEQLKDVVANNANWFSRAVKVLADIFVPLIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                 MDHXDLAQRILRDIGGEDNIVAAAHCATRLRLVLKDTKDVDRQSLDDDPDLKGTFETGGM
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                                                                                                   KRFGGNPFLGAALGMILVHPSLMSAYDFPKAVEAGKAIPYWDVFGLHINQVGYQGQVLPM
                                                                                                                                               KRFGGNEFLGAGIGMAMVFPTLVNGYDVAATMTAGE-MPMWSLFGLDVAQAGYQGTVLPV
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Pred. No. 3.1e-63;
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RT "Complete genomes of two clinical Staphylococcus aureus strains: RT evidence for the rapid evolution of virulence and drug resistance."; REMBL; BX571857; CA6444082.1; -

RGO; GO:0016020; C:membrane; IEA.

DR GO; GO:0016325; F:sugar porter activity; IEA.

GO; GO:0016326; F:sugar porter activity; IEA.

GO; GO:0005351; F:sugar porter activity; IEA.

DR GO; GO:0005352; Ptrans EIIB.

RGO; GO:0006810; P:transferase activity; IEA.

DR GO; GO:0016310; P:transferase activity; IEA.

DR GO; GO:0016310; P:TS EIIB; 1.

DR Pfam; PF00378; PTS EIIB; 1.

DR Ffam; PF00378; PTS EIIB; 1.

DR Ffam; PF00378; PTS EIIB; 1.

DR Ffam; PF00378; PTS EIIB; 1.

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DR FGDR FF EIIB; 1.

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Best Local S
Matches 242
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Bacteria; Firmicutes; Bacillales; Stap
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OrderedLocusNames=SAS2269;
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27, Last annotation (EC ?
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                                                                                                                                                              Score 1183;
Pred. No. 3
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RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst I., Atkin R., Barron A.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst I., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Churcher C., Harris B., Hauser H., Holroyd S., Jagels K.,
Ra Entwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
Ra Entwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
Ra Entwell T., Hance Z., Harris B., Rutherford K.M., Sanders M.,
Ra Entwell T., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Ra Entwell T., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
Ra Entwell T., Parkhill J.;
Reproc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
                                                                                                                                 REMBL; BX571856; CAG41448.1; -...

REGO; GO:0016020; C:membrane; IEA.

REGO; GO:0008982; F:protein-N(FI)-phosphohistidine-sugar phosph...

REGO; GO:0008982; F:protein-N(FI)-phosphohistidine-sugar phosph...

REGO; GO:0008401; F:sugar porter activity; IEA.

REGO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho...

REGO; GO:0009401; P:transport; IEA.

REGO; GO:0009401; P:transport; IEA.

REGO; GO:0009401; P:transport; IEA.

REGO; GO:00091355; EIIB 91C.

REINTERPRO; IPR001996; PTS-EIIB; 1.

REGO; FOO367; PTS_EIIB; 1.

REGO; GO:0009401; PTS_EIIB; 1.

REGO; GO:0009401; PTS_EIIB; 1.

REGO; GO:0009401; PTS_EIIB; 1.

REGO; GO:0009401; PTS_EIIB; 1.

REGO; GO:0009401; PTS_EIIB; 1.

REGO; GO:0009401; PTS_EIIB; 1.

REGO; GO:0009401; PTS_EIIB; 1.

REGO; GO:0009401; PTS_EIIB; 1.

REGO; GO:0009401; PTS_EIIB; 1.

REGOSTITE; PTGR001996; PTS-II-BC-sucr; 1.

REGOSTITE; PS01035; PTS_EIIB_CYS; 1.
Query Match
Best Local Similarity
                                                                                        Complete
SEQUENCE
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Bacteria; Firmicutes; Bacillales; Staphylococcus
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D 099R00

C 099R00

JT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 26, Last annotation update)

DT 978 system, sucrose-specific IIBC component.

GN Name-scra; OrderedlocusNames-SAV2377;

OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Mu50 / ATCC 700699;
MEDLINE=21311952; PubMed=11418146;
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Best Local Similarity
Matches 242; Conserv
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ProDom; PD001476; Ptrans_EIIB; 1.
TIGRPAMS; TIGR00826; EIIB glc; 1.
TIGRPAMS; TIGR01996; PTS-II-BC-sucr;
PROSITS; PS01035; PTS_EIIB_CYS; 1.
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                                                         AACLAVFFLAK-SEKLKGLAGASGVSAVLGITEPAIFGVNLRLRWPFYIGIGTAAIGGAL
                                                                                           LYEFGGAIGGLIFGLLYAPIVITGMHSPIAVETTLIADATKTGGSPIFPIATMSNVAQG
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Search completed: March 7, 2005, 22:14:08 Job time: 183 secs

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